GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:05:30 ; Search time 81 Seconds
(without alignments)
19.596 Million cell updates/sec

Title: US-09-103-808-1
Perfect score: 65
Sequence: 1 YSWMDISCWI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 251420

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	10	18	AAW16576	Human gastric canc
2	65	100.0	10	21	AAY54325	Peptide used to de
3	65	100.0	10	23	ABG79110	Human HST-2 class
4	61	93.8	9	18	AAW16577	Human gastric canc
5	32	49.2	8	22	ABP15183	HIV A24 super moti
6	32	49.2	8	22	ABP24036	HIV A24 motif env
7	32	49.2	9	22	ABP15292	HIV A24 super moti
8	32	49.2	9	22	ABP15394	HIV A24 super moti
9	32	49.2	9	22	ABP15485	HIV A24 super moti
10	32	49.2	9	22	ABP19698	HIV A01 motif env
11	32	49.2	9	22	ABP19896	HIV A03 motif env
12	32	49.2	9	22	ABP22345	HIV A11 motif env
13	32	49.2	9	22	ABP24037	HIV A24 motif env
14	32	49.2	9	22	ABP24040	HIV A24 motif env
15	31	47.7	9	22	AAB66551	Phage clone ed1 pI
16	30	46.2	8	22	AAB78533	SIV gp 41 enhancer
17	30	46.2	10	24	AAE32600	West nile virus (W
18	29	44.6	5	5	AAP40008	Sequence of gastri
19	29	44.6	7	5	AAP40033	Sequence of gastri
20	29	44.6	7	6	AAP50373	Gastric acid secre
21	29	44.6	7	21	AAY51308	Human gastrin G17
22	29	44.6	8	6	AAP50374	Gastric acid secre
23	29	44.6	8	16	AAR79689	pp60(c-src) kinase
24	29	44.6	8	21	AAY57990	Gastrin peptide SE
25	29	44.6	9	16	AAR79712	EGF receptor Tyr k
26	29	44.6	9	21	AAY67913	Gastrin peptide SE
27	29	44.6	10	15	AAR73750	Antigen fragment 6
28	29	44.6	10	22	AAB46952	Synthetic gastrin
29	29	44.6	10	23	ABG98798	F protein decapept
30	29	44.6	10	23	ABG98799	F protein decapept
31	28	43.1	6	22	AAB49571	RT-loop peptide fr
32	28	43.1	10	19	AAW70084	S. cerevisiae meth
33	27.5	42.3	10	22	AAG96187	Human complementar
34	27.5	42.3	10	22	AAG96189	Human complementar
35	27.5	42.3	10	22	AAG96221	Human complementar
36	27.5	42.3	10	22	AAG96223	Human complementar
37	27	41.5	7	14	AAR38734	WWamide 1. Achati
38	27	41.5	8	23	ABJ06730	Hepatitis B virus
39	27	41.5	8	23	ABJ08663	Hepatitis B virus
40	27	41.5	9	15	AAR59139	Peptide fragment (
41	27	41.5	9	18	AAW13439	Brain homing pepti
42	27	41.5	9	20	AAY46033	Immunogenic peptid
43	27	41.5	9	20	AAY46441	Immunogenic peptid
44	27	41.5	9	20	AAY46498	Immunogenic peptid
45	27	41.5	9	21	AAM49132	Hepatitis B virus

ALIGNMENTS

RESULT 1
AAW16576
ID AAW16576 standard; peptide; 10 AA.
XX
AC AAW16576;
XX
DT 27-JAN-1998 (first entry)
XX
DE Human gastric cancer antigen fragment 1.
XX
KW Gastric cancer; gastric cancer antigen; human leukocyte antigen;
KW HLA; cytotoxic T lymphocyte; CTL; recombinant bacterium;
KW recombinant virus; gastric cancer; vaccine.
XX
OS Homo sapiens.
XX
PN EP770624-A2.
XX
PD 02-MAY-1997.
XX
PF 30-SEP-1996; 96EP-0307163.
XX
PR 19-AUG-1996; 96JP-0217140.
PR 29-SEP-1995; 95JP-0253491.
XX
PA (AJIN) AJINOMOTO CO INC.
PA (KIKU/) KIKUCHI K.
XX
PI Hamuro J, Kikuchi K, Sahara H, Sato N, Suzuki M;
PI Wada Y, Yasojima T;
XX
DR WPI; 1997-238096/22.

XX
PT Gastric cancer antigen fragment present in human gastric cancer cell
PT - induces cytotoxic T lymphocyte response when bound to human
PT leukocyte antigen, for gastric cancer treatment or prevention
XX
PS Claim 3; Page 9; 14pp; English.
XX
CC This novel peptide is a fragment of a gastric cancer antigen present in
CC a human gastric cancer cell, which when bound to a human leukocyte
CC antigen (HLA), is capable of inducing a cytotoxic T lymphocyte (CTL)
CC response that targets the gastric cancer cell. A second peptide
CC (AAW16577) has also been produced, containing amino acids 1-9 of the
CC present sequence. However, peptides containing amino acids 1-8 and 1-7 of
CC the present sequence have no CTL inducibility, and cannot be used. The
CC HLA-bound peptides can be used to treat or prevent gastric cancer.
CC Viruses, e.g. vaccinia virus, or bacteria, e.g. BCG, which contain the
CC DNA encoding this peptide can be used as a live vaccine for preventing
CC or treating human gastric cancer.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 65; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCWI 10
||||||||||
Db 1 YSWMDISCWI 10

RESULT 2
AAY54325
ID AAY54325 standard; Peptide; 10 AA.
XX
AC AAY54325;
XX
DT 06-APR-2000 (first entry)
XX
DE Peptide used to design a probe to screen for gastric cancer antigen gene.
XX
KW Human; gastric cancer antigen; cytotoxic T cell response; gastric cancer;
KW HLA-A31 antigen; tumour antigen; vaccine.
XX
OS Homo sapiens.
XX
PN EP974653-A2.
XX
PD 26-JAN-2000.
XX
PF 09-JUL-1999; 99EP-0305469.
XX
PR 13-JUL-1998; 98JP-0197852.
XX
PA (AJIN) AJINOMOTO CO INC.
PA (KIKU/) KIKUCHI K.
XX
PI Kikuchi K, Sato N, Torigoe T, Sahara H, Suzuki M, Hamuro J;
XX
DR WPI; 2000-108398/10.
DR N-PSDB; AAZ45610.
XX
PT New antigen proteins, useful for the prevention and treatment of human
PT gastric cancer -
XX
PS Example 2; Page 10; 13pp; English.
XX
CC The present sequence represents a peptide (peptide F4.2) used to
CC design a probe to screen for a human gastric cancer antigen gene.
CC The gastric cancer antigen polypeptide induces a cytotoxic T cell
CC response against human gastric cancer cells, by binding to HLA-A31
CC antigen expressed by gastric cancer cells. The tumour antigen gene
CC was identified by screening a cDNA library derived from a gastric
CC cancer cell line that can induce a gastric cancer antigen specific
CC cytotoxic T cell response. The gastric cancer antigen polynucleotide
CC can be used in a recombinant virus or bacterium as a vaccine. The
CC gastric cancer antigen polypeptides are also used for the prevention
CC or treatment of human gastric cancer.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 65; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCWI 10
||||||||||
Db 1 YSWMDISCWI 10

RESULT 3
ABG79110
ID ABG79110 standard; Peptide; 10 AA.
XX
AC ABG79110;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human HST-2 class I HLA tumour-restricted antigen peptide.
XX
KW Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;
KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;
KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;
KW ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell;
KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
KW cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO200264057-A2.
XX
PD 22-AUG-2002.
XX
PF 15-FEB-2002; 2002WO-US05212.
XX
PR 15-FEB-2001; 2001US-268687P.
XX
PA (BAYU) BAYLOR COLLEGE MEDICINE.
XX
PI Wang R;
XX
DR WPI; 2002-627577/67.
XX
PT Novel composition for treating a disease in an animal, comprises an
PT immune effector cell and cell penetrating peptide associated with an
PT antigen or antibody -
XX
PS Disclosure; Page 20; 61pp; English.
XX
CC The invention relates to a composition (I) comprising an immune effector
CC cell and a cell penetrating peptide (CPP) associated with an antigen or
CC antibody. Also included are (1) a vaccine comprising (I), CPP
CC associated with an antigen, and a pharmaceutically acceptable carrier
CC and (2) preparing a composition for a disease, by providing (I)
CC and CPP associated with an antigen for disease, and introducing the
CC antigen-associated CPP to (I), where antigen enters into the cell.
CC The antigens are, for example, tumour antigen derived epitopes
CC recognised by tumour infiltrating lymphocytes (TIL) of HLA (human
CC leukocyte antigen) class I or II. The composition is useful for enhancing
CC immunity in an animal to a disease, by administering a mature dendritic
CC cell comprising CPP associated with an antigen to disease, to the animal,
CC such that following the administration, animal is protected from disease,
CC where the animal comprises both CD4+ and CD8+ T cells. It is also useful
CC for treating a disease (e.g. cancer, tumour, melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia,
CC Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer,

CC kidney cancer, adenocarcinoma, breast cancer, prostate cancer,
CC ovarian cancer and pancreatic cancer). The animal is further subjected to
CC a cancer treatment including surgery, radiation, chemotherapy or gene
CC therapy. The administration of (I), preferably dendritic cell is prior
CC to, subsequent to or concurrent with, the cancer treatment. The present
CC sequence is a tumour antigen derived epitope for inclusion in the
CC composition of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 65; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCWI 10
||||||||||
Db 1 YSWMDISCWI 10

RESULT 4
AAW16577
ID AAW16577 standard; peptide; 9 AA.
XX
AC AAW16577;
XX
DT 27-JAN-1998 (first entry)
XX
DE Human gastric cancer antigen fragment 2.
XX
KW Gastric cancer; gastric cancer antigen; human leukocyte antigen;
KW HLA; cytotoxic T lymphocyte; CTL; recombinant bacterium;
KW recombinant virus; gastric cancer; vaccine.
XX
OS Homo sapiens.
XX
PN EP770624-A2.
XX
PD 02-MAY-1997.
XX
PF 30-SEP-1996; 96EP-0307163.
XX
PR 19-AUG-1996; 96JP-0217140.
PR 29-SEP-1995; 95JP-0253491.
XX
PA (AJIN) AJINOMOTO CO INC.
PA (KIKU/) KIKUCHI K.
XX
PI Hamuro J, Kikuchi K, Sahara H, Sato N, Suzuki M;
PI Wada Y, Yasojima T;
XX
DR WPI; 1997-238096/22.
XX
PT Gastric cancer antigen fragment present in human gastric cancer cell
PT - induces cytotoxic T lymphocyte response when bound to human
PT leukocyte antigen, for gastric cancer treatment or prevention
XX
PS Claim 5; Page 9; 14pp; English.
XX
CC This novel peptide is a fragment of a gastric cancer antigen present in
CC a human gastric cancer cell, which when bound to a human leukocyte
CC antigen (HLA), is capable of inducing a cytotoxic T lymphocyte (CTL)
CC response that targets the gastric cancer cell. It is based on amino acids
CC 1-9 of peptide 1 (AAW16576), whih shows the same effect. However,
CC peptides containing amino acids 1-8 and 1-7 of peptide 1 have no CTL
CC inducibility, and cannot be used. The HLA-bound peptides can be used to
CC treat or prevent gastric cancer. Viruses, e.g. vaccinia virus, or
CC bacteria, e.g. BCG, which contain the DNA encoding this peptide can be
CC used as a live vaccine for preventing or treating human gastric cancer.
XX
SQ Sequence 9 AA;

Query Match 93.8%; Score 61; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCW 9
|||||||||
Db 1 YSWMDISCW 9

RESULT 5
ABP15183
ID ABP15183 standard; Peptide; 8 AA.
XX
AC ABP15183;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #63.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 180; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;

Query Match 49.2%; Score 32; DB 22; Length 8;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCWI 10

```
              | ||: |:
Db          1 WFDITNWL 8


RESULT 6
ABP24036
ID   ABP24036 standard; Peptide; 8 AA.
XX
AC   ABP24036;
XX
DT   15-JUL-2002  (first entry)
XX
DE   HIV A24 motif env peptide #2.
XX
KW   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW   vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW   antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200124810-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US27766.
XX
PR   05-OCT-1999;   99US-0412863.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Sidney J,  Southwood S,  Livingston BD,  Chesnut R;
PI   Baker DM,  Celis E,  Kubo RT,  Grey HM;
XX
DR   WPI; 2001-354887/37.
XX
PT   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT   peptide groups, useful for vaccinating against HIV-1 -
XX
PS   Claim 32; Page 362; 448pp; English.
XX
CC   The present invention describes a composition (I) comprising a prepared
CC   human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC   sequence selected from 51 defined amino acid sequences (ABL25347 to
CC   ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC   may be used for immunising subjects against HIV-1 infections. The use of
CC   group-based vaccines has several advantages over traditional vaccines,
CC   particularly when compared to the use of whole antigens in vaccine
CC   compositions. There is evidence that the immune response to whole
CC   antigens is directed largely toward variable regions of the antigen,
CC   allowing for immune escape due to mutations. The groups for inclusion in
CC   an group-based vaccine may be selected from conserved regions of viral or
CC   tumour-associated antigens, which therefore reduces the likelihood of
CC   escape mutants. Furthermore, immunosuppressive groups that may be present
CC   in whole antigens can be avoided with the use of group-based vaccines.
CC   An additional advantage of an group-based vaccine approach is the ability
CC   to combine selected groups (CTL and HTL), and further, to modify the
CC   composition of the groups, achieving, for example, enhanced
CC   immunogenicity. Accordingly, the immune response can be modulated, as
CC   appropriate, for the target disease. Similar engineering of the response
CC   is not possible with traditional approaches. ABP11501 to ABP25412
CC   represent peptide sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   8 AA;

  Query Match             49.2%;  Score 32;  DB 22;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||: |:
Db          1 WFDITNWL 8


RESULT 7
ABP15292
ID   ABP15292 standard; Peptide; 9 AA.
XX
AC   ABP15292;
XX
DT   15-JUL-2002  (first entry)
XX
DE   HIV A24 super motif env peptide #172.
XX
KW   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW   vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW   antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200124810-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US27766.
XX
PR   05-OCT-1999;   99US-0412863.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Sidney J,  Southwood S,  Livingston BD,  Chesnut R;
PI   Baker DM,  Celis E,  Kubo RT,  Grey HM;
XX
DR   WPI; 2001-354887/37.
XX
PT   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT   peptide groups, useful for vaccinating against HIV-1 -
XX
PS   Claim 32; Page 182; 448pp; English.
XX
CC   The present invention describes a composition (I) comprising a prepared
CC   human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC   sequence selected from 51 defined amino acid sequences (ABL25347 to
CC   ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC   may be used for immunising subjects against HIV-1 infections. The use of
CC   group-based vaccines has several advantages over traditional vaccines,
CC   particularly when compared to the use of whole antigens in vaccine
CC   compositions. There is evidence that the immune response to whole
CC   antigens is directed largely toward variable regions of the antigen,
CC   allowing for immune escape due to mutations. The groups for inclusion in
CC   an group-based vaccine may be selected from conserved regions of viral or
CC   tumour-associated antigens, which therefore reduces the likelihood of
CC   escape mutants. Furthermore, immunosuppressive groups that may be present
CC   in whole antigens can be avoided with the use of group-based vaccines.
CC   An additional advantage of an group-based vaccine approach is the ability
CC   to combine selected groups (CTL and HTL), and further, to modify the
CC   composition of the groups, achieving, for example, enhanced
CC   immunogenicity. Accordingly, the immune response can be modulated, as
CC   appropriate, for the target disease. Similar engineering of the response
CC   is not possible with traditional approaches. ABP11501 to ABP25412
CC   represent peptide sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   9 AA;

  Query Match             49.2%;  Score 32;  DB 22;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||: |:
Db          1 WFDITNWL 8


RESULT 8
ABP15394
```

ID ABP15394 standard; Peptide; 9 AA.
XX
AC ABP15394;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #274.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 184; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 32; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCWI 10
| ||: |:
Db 1 WFDITNWL 8

RESULT 9
ABP15485
ID ABP15485 standard; Peptide; 9 AA.
XX
AC ABP15485;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #365.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 186; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 32; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCWI 10
| ||: |:
Db 1 WFDITNWL 8

RESULT 10
ABP19698
ID ABP19698 standard; Peptide; 9 AA.
XX
AC ABP19698;
XX
DT 15-JUL-2002 (first entry)
XX

DE HIV A01 motif env peptide #8.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 273; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 32; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCWI 10
| ||: |:
Db 1 WFDITNWL 8

RESULT 11
ABP19896
ID ABP19896 standard; Peptide; 9 AA.
XX
AC ABP19896;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A03 motif env peptide #100.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 277; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 32; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCWI 10
| ||: |:
Db 1 WFDITNWL 8

RESULT 12
ABP22345
ID ABP22345 standard; Peptide; 9 AA.
XX
AC ABP22345;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A11 motif env peptide #68.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX

OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 327; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

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  Query Match             49.2%;  Score 32;  DB 22;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||: |:
Db          1 WFDITNWL 8
```

RESULT 13
ABP24037
ID ABP24037 standard; Peptide; 9 AA.
XX
AC ABP24037;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 motif env peptide #3.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 362; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

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  Query Match             49.2%;  Score 32;  DB 22;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||: |:
Db          1 WFDITNWL 8
```

RESULT 14
ABP24040
ID ABP24040 standard; Peptide; 9 AA.
XX
AC ABP24040;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 motif env peptide #6.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX

PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 362; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 32; DB 22; Length 9;
Best Local Similarity 50.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCWI 10
| ||: |:
Db 1 WFDITNWL 8

RESULT 15
AAB66551
ID AAB66551 standard; peptide; 9 AA.
XX
AC AAB66551;
XX
DT 10-APR-2001 (first entry)
XX
DE Phage clone ed1 pIII-displayed peptide.
XX
KW phage display; antianaemic; cytostatic; immunosuppressive;
KW immunoglobulin M; IgM; IgM binding; autoimmune haemolytic anaemia;
KW paraneoplastic syndrome; multiple myeloma; cancer; autoimmune disease.
XX
OS Synthetic.
XX
PN WO200102001-A1.
XX
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-US18320.
XX
PR 02-JUL-1999; 99US-0142048.
PR 06-JUL-1999; 99US-0142389.
PR 07-JUL-1999; 99US-0142524.
XX
PA (RERE-) RES & DEV INST INC.
XX
PI Glee PM, Pincus SH, Burritt JB, Cutler JE;
XX
DR WPI; 2001-138063/14.
XX
PT Novel peptides that bind to immunoglobulin M antibodies and block their
PT interaction with antigens, useful for treating rheumatoid factor biding
PT to immunoglobulin G, autoimmune hemolytic anemia or paraneoplastic
PT syndromes -
XX
PS Claim 10; Page 6; 60pp; English.
XX
CC The present sequence is one of a number of random 9-mer peptides which
CC were displayed from the N-terminal portion of the pIII capsid protein of
CC filamentous bacteriophage M13KBst. Peptides that selectively bind to
CC immunoglobulin (Ig)M antibodies but do not selectively bind to antibodies
CC of other classes were identified. Such peptides are useful for detecting
CC the presence of IgM in a sample and for purifying IgM from a sample.
CC The peptides are also useful for isolating an antigen specific IgM
CC population or for isolating an antigen bound by a specific IgM
CC population. They are useful for treating a human disease associated with
CC IgM antibodies such as rheumatoid factor binding to IgG,
CC isohaemagglutinin binding to red blood cells, autoimmune haemolytic
CC anaemia, paraneoplastic syndromes, multiple myeloma or cancer.
CC The peptides are useful for treating diseases such as cancer or an
CC autoimmune disease associated with IgM antibodies by removing IgM from
CC serum. The peptides are capable of selectively binding to the IgM
CC molecules of several mammalian species and to both the pentameric and
CC monomeric forms of IgM molecules.
XX
SQ Sequence 9 AA;

Query Match 47.7%; Score 31; DB 22; Length 9;
Best Local Similarity 44.4%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YSWMDISCW 9
| |: | |
Db 1 YDWIPSSAW 9

Search completed: August 4, 2003, 12:15:16
Job time : 83 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:13:55 ; Search time 29 Seconds
(without alignments)
14.590 Million cell updates/sec

Title: US-09-103-808-1
Perfect score: 65
Sequence: 1 YSWMDISCWI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 90058

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	10	2	US-08-723-116-1	Sequence 1, Appli
2	65	100.0	10	4	US-09-103-808-1	Sequence 1, Appli
3	65	100.0	10	4	US-09-348-265-3	Sequence 3, Appli
4	61	93.8	9	2	US-08-723-116-2	Sequence 2, Appli
5	61	93.8	9	4	US-09-103-808-2	Sequence 2, Appli
6	50	76.9	8	2	US-08-723-116-3	Sequence 3, Appli
7	50	76.9	8	4	US-09-103-808-3	Sequence 3, Appli
8	41	63.1	7	2	US-08-723-116-4	Sequence 4, Appli
9	41	63.1	7	4	US-09-103-808-4	Sequence 4, Appli
10	30	46.2	7	1	US-08-431-539-9	Sequence 9, Appli
11	30	46.2	8	3	US-09-082-279B-1480	Sequence 1480, Ap
12	30	46.2	8	4	US-09-315-304B-1634	Sequence 1634, Ap
13	30	46.2	8	4	US-09-834-784-1480	Sequence 1480, Ap
14	29	44.6	6	1	US-08-431-539-11	Sequence 11, Appl
15	29	44.6	7	1	US-08-431-539-15	Sequence 15, Appl
16	29	44.6	8	1	US-08-178-570-44	Sequence 44, Appl
17	29	44.6	8	3	US-08-369-643-44	Sequence 44, Appl
18	29	44.6	8	5	PCT-US95-00147-44	Sequence 44, Appl
19	29	44.6	9	1	US-08-178-570-69	Sequence 69, Appl
20	29	44.6	9	3	US-08-369-643-69	Sequence 69, Appl
21	29	44.6	9	5	PCT-US95-00147-69	Sequence 69, Appl
22	28	43.1	10	1	US-08-584-226-21	Sequence 21, Appl
23	27	41.5	9	1	US-08-526-710-13	Sequence 13, Appl
24	27	41.5	9	3	US-08-862-855-13	Sequence 13, Appl
25	27	41.5	9	3	US-09-226-985-13	Sequence 13, Appl
26	27	41.5	9	4	US-09-227-906-13	Sequence 13, Appl
27	27	41.5	9	4	US-09-311-784A-222	Sequence 222, App
28	26	40.0	5	2	US-08-559-492-6	Sequence 6, Appli
29	26	40.0	7	3	US-09-059-111-16	Sequence 16, Appl
30	26	40.0	7	3	US-09-059-111-39	Sequence 39, Appl
31	26	40.0	7	5	PCT-US95-08353-16	Sequence 16, Appl
32	26	40.0	7	5	PCT-US95-08353-39	Sequence 39, Appl
33	26	40.0	8	1	US-08-271-830-55	Sequence 55, Appl
34	26	40.0	9	3	US-09-258-754-64	Sequence 64, Appl
35	26	40.0	9	3	US-09-042-107-64	Sequence 64, Appl
36	26	40.0	10	3	US-08-159-339A-469	Sequence 469, App
37	25	38.5	6	3	US-09-059-111-24	Sequence 24, Appl
38	25	38.5	6	5	PCT-US95-08353-24	Sequence 24, Appl
39	25	38.5	8	1	US-08-190-788A-18	Sequence 18, Appl
40	25	38.5	8	1	US-08-383-474B-23	Sequence 23, Appl
41	25	38.5	8	1	US-08-465-391A-18	Sequence 18, Appl
42	25	38.5	8	2	US-08-464-538B-18	Sequence 18, Appl
43	25	38.5	8	2	US-08-463-076E-62	Sequence 62, Appl
44	24.5	37.7	8	3	US-08-907-403A-4	Sequence 4, Appli
45	24	36.9	5	2	US-08-757-316C-28	Sequence 28, Appl

ALIGNMENTS

```
RESULT 1
US-08-723-116-1
; Sequence 1, Application US/08723116
; Patent No. 5837248
;  GENERAL INFORMATION:
;    APPLICANT:  KIKUCHI, KOKICHI
;    APPLICANT:  SATO, NORIYUKI
;    APPLICANT:  SAHARA, HIROMITSU
;    APPLICANT:  YASOJIMA, TAKAHIRO
;    APPLICANT:  WADA, YOSHIMASA
;    APPLICANT:  SUZUKI, MANABU
;    APPLICANT:  HAMURO, JUNJI
;    TITLE OF INVENTION:  PEPTIDE CAPABLE OF INDUCING IMMUNE
;    TITLE OF INVENTION:  RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;    TITLE OF INVENTION:  OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,116
;      FILING DATE:  30-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 253491/1995
;      FILING DATE:  29-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 217140/1996
;      FILING DATE:  19-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-821-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
US-08-723-116-1

Query Match 100.0%; Score 65; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCWI 10
||||||||||
Db 1 YSWMDISCWI 10

RESULT 2
US-09-103-808-1
; Sequence 1, Application US/09103808
; Patent No. 6368852
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; SATO, NORIYUKI
; SAHARA, HIROMITSU
; YASOJIMA, TAKAHIRO
; WADA, YOSHIMASA
; SUZUKI, MANABU
; HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,808
; FILING DATE: 24-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,116
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-103-808-1

Query Match 100.0%; Score 65; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCWI 10
||||||||||
Db 1 YSWMDISCWI 10

RESULT 3
US-09-348-265-3
; Sequence 3, Application US/09348265
; Patent No. 6444800
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Kokichi
; APPLICANT: SATO, No. 6444800iyuki
; APPLICANT: TORIGOE, Toshihiko
; APPLICANT: SAHARA, Hiroeki
; APPLICANT: SUZUKI, Manabu
; APPLICANT: HAMURO, Junji
; TITLE OF INVENTION: Human Gastric Cancer Antigen Gene and Gastric
; TITLE OF INVENTION: Cancer Antigen Protein
; FILE REFERENCE: OP871
; CURRENT APPLICATION NUMBER: US/09/348,265
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 10-197852
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-265-3

Query Match 100.0%; Score 65; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCWI 10
||||||||||
Db 1 YSWMDISCWI 10

RESULT 4
US-08-723-116-2
; Sequence 2, Application US/08723116
; Patent No. 5837248
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, KOKICHI
; APPLICANT: SATO, NORIYUKI
; APPLICANT: SAHARA, HIROMITSU
; APPLICANT: YASOJIMA, TAKAHIRO
; APPLICANT: WADA, YOSHIMASA
; APPLICANT: SUZUKI, MANABU
; APPLICANT: HAMURO, JUNJI
; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; TITLE OF INVENTION: RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; TITLE OF INVENTION: OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,116
;      FILING DATE:  30-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 253491/1995
;      FILING DATE:  29-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 217140/1996
;      FILING DATE:  19-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-821-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN
US-08-723-116-2

  Query Match             93.8%;  Score 61;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISCW 9
              |||||||||
Db          1 YSWMDISCW 9


RESULT 5
US-09-103-808-2
; Sequence 2, Application US/09103808
; Patent No. 6368852
;  GENERAL INFORMATION:
;       APPLICANT: KIKUCHI, KOKICHI
;                  SATO, NORIYUKI
;                  SAHARA, HIROMITSU
;                  YASOJIMA, TAKAHIRO
;                  WADA, YOSHIMASA
;                  SUZUKI, MANABU
;                  HAMURO, JUNJI
;       TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
;                           RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;                           OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;                       P.C.
;            STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;            CITY: ARLINGTON
;            STATE: VA
;            COUNTRY: USA
;            ZIP: 22202
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/103,808
;            FILING DATE: 24-Jun-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/723,116
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: JP 217140/1996
;            FILING DATE: 19-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: OBLON, NORMAN F.
;            REGISTRATION NUMBER: 24,618
;            REFERENCE/DOCKET NUMBER: 10-821-0X
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 703-413-3000
;            TELEFAX: 703-413-2220
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 9 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       ORIGINAL SOURCE:
;            ORGANISM: HUMAN
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-103-808-2

  Query Match             93.8%;  Score 61;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISCW 9
              |||||||||
Db          1 YSWMDISCW 9


RESULT 6
US-08-723-116-3
; Sequence 3, Application US/08723116
; Patent No. 5837248
;  GENERAL INFORMATION:
;    APPLICANT:  KIKUCHI, KOKICHI
;    APPLICANT:  SATO, NORIYUKI
;    APPLICANT:  SAHARA, HIROMITSU
;    APPLICANT:  YASOJIMA, TAKAHIRO
;    APPLICANT:  WADA, YOSHIMASA
;    APPLICANT:  SUZUKI, MANABU
;    APPLICANT:  HAMURO, JUNJI
;    TITLE OF INVENTION:  PEPTIDE CAPABLE OF INDUCING IMMUNE
;    TITLE OF INVENTION:  RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;    TITLE OF INVENTION:  OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,116
;      FILING DATE:  30-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 253491/1995
;      FILING DATE:  29-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 217140/1996
;      FILING DATE:  19-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-821-0X
```

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;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN
US-08-723-116-3

  Query Match             76.9%;  Score 50;  DB 2;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISC 8
              ||||||||
Db          1 YSWMDISC 8


RESULT 7
US-09-103-808-3
; Sequence 3, Application US/09103808
; Patent No. 6368852
;  GENERAL INFORMATION:
;       APPLICANT: KIKUCHI, KOKICHI
;                  SATO, NORIYUKI
;                  SAHARA, HIROMITSU
;                  YASOJIMA, TAKAHIRO
;                  WADA, YOSHIMASA
;                  SUZUKI, MANABU
;                  HAMURO, JUNJI
;       TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
;                           RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;                           OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;                       P.C.
;            STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;            CITY: ARLINGTON
;            STATE: VA
;            COUNTRY: USA
;            ZIP: 22202
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/103,808
;            FILING DATE: 24-Jun-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/723,116
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: JP 217140/1996
;            FILING DATE: 19-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: OBLON, NORMAN F.
;            REGISTRATION NUMBER: 24,618
;            REFERENCE/DOCKET NUMBER: 10-821-0X
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 703-413-3000
;            TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 8 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;          MOLECULE TYPE: peptide
;          ORIGINAL SOURCE:
;               ORGANISM: HUMAN
;          SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-103-808-3

  Query Match             76.9%;  Score 50;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISC 8
              ||||||||
Db          1 YSWMDISC 8


RESULT 8
US-08-723-116-4
; Sequence 4, Application US/08723116
; Patent No. 5837248
;  GENERAL INFORMATION:
;    APPLICANT:  KIKUCHI, KOKICHI
;    APPLICANT:  SATO, NORIYUKI
;    APPLICANT:  SAHARA, HIROMITSU
;    APPLICANT:  YASOJIMA, TAKAHIRO
;    APPLICANT:  WADA, YOSHIMASA
;    APPLICANT:  SUZUKI, MANABU
;    APPLICANT:  HAMURO, JUNJI
;    TITLE OF INVENTION:  PEPTIDE CAPABLE OF INDUCING IMMUNE
;    TITLE OF INVENTION:  RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;    TITLE OF INVENTION:  OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,116
;      FILING DATE:  30-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 253491/1995
;      FILING DATE:  29-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 217140/1996
;      FILING DATE:  19-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-821-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN
US-08-723-116-4
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  Query Match             63.1%;  Score 41;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDIS 7
              |||||||
Db          1 YSWMDIS 7


RESULT 9
US-09-103-808-4
; Sequence 4, Application US/09103808
; Patent No. 6368852
;   GENERAL INFORMATION:
;       APPLICANT: KIKUCHI, KOKICHI
;                  SATO, NORIYUKI
;                  SAHARA, HIROMITSU
;                  YASOJIMA, TAKAHIRO
;                  WADA, YOSHIMASA
;                  SUZUKI, MANABU
;                  HAMURO, JUNJI
;       TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
;                           RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;                           OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;                       P.C.
;            STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;            CITY: ARLINGTON
;            STATE: VA
;            COUNTRY: USA
;            ZIP: 22202
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/103,808
;            FILING DATE: 24-Jun-1998
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/723,116
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: JP 217140/1996
;            FILING DATE: 19-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: OBLON, NORMAN F.
;            REGISTRATION NUMBER: 24,618
;            REFERENCE/DOCKET NUMBER: 10-821-0X
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 703-413-3000
;            TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 7 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       ORIGINAL SOURCE:
;            ORGANISM: HUMAN
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-103-808-4

  Query Match             63.1%;  Score 41;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDIS 7
              |||||||
Db          1 YSWMDIS 7


RESULT 10
US-08-431-539-9
; Sequence 9, Application US/08431539
; Patent No. 5580751
;  GENERAL INFORMATION:
;    APPLICANT:  Buchardt, Ole
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Henriksen, Dennis
;    TITLE OF INVENTION:  Process for the Preparation of
;    TITLE OF INVENTION:  C-Terminally Amidated Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 No. 5580751west Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,539
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,306
;      FILING DATE:  15-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelson, Albin J.
;      REGISTRATION NUMBER:  28,650
;      REFERENCE/DOCKET NUMBER:  9663.8-US-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-431-539-9

  Query Match             46.2%;  Score 30;  DB 1;  Length 7;
  Best Local Similarity   57.1%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YSWMDIS 7
              | |||  :
Db          1 YGWMDFA 7


RESULT 11
US-09-082-279B-1480
; Sequence 1480, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
;  APPLICANT:  Barney, Shawn
;  APPLICANT:  Guthrie, Kelly
;  APPLICANT:  Merutka, Gene
;  APPLICANT:  Anwer, Mohmed
;  APPLICANT:  Lambert, Dennis
;  TITLE OF INVENTION:  HYBRID POLYPEPTIDES WITH ENHANCED
;  TITLE OF INVENTION:  PHARMACOKINETIC PROPERTIES
;  FILE REFERENCE:  7872-043
;  CURRENT APPLICATION NUMBER: US/09/082,279B
;  CURRENT FILING DATE:  1998-05-20
;  NUMBER OF SEQ ID NOS:  1515
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;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1480
;    LENGTH: 8
;    TYPE: PRT
;    ORGANISM: SIV
US-09-082-279B-1480

  Query Match             46.2%;  Score 30;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||   |:
Db          1 WSDIWSWV 8


RESULT 12
US-09-315-304B-1634
; Sequence 1634, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
;  APPLICANT: Barney, S.
;  APPLICANT:  Guthrie, K.
;  APPLICANT:  Merutka, G.
;  APPLICANT:  Anwer, M.
;  APPLICANT:  Lambert, D.
;  TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
;  TITLE OF INVENTION:  PROPERTIES
;  FILE REFERENCE: 7872-052
;  CURRENT APPLICATION NUMBER: US/09/315,304B
;  CURRENT FILING DATE:  1999-05-20
;  PRIOR APPLICATION NUMBER: 09/082,279
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 1667
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1634
;    LENGTH: 8
;    TYPE: PRT
;    ORGANISM: SIV
US-09-315-304B-1634

  Query Match             46.2%;  Score 30;  DB 4;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||   |:
Db          1 WSDIWSWV 8


RESULT 13
US-09-834-784-1480
; Sequence 1480, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
;  APPLICANT: Barney, Shawn
;  APPLICANT:  Guthrie, Kelly
;  APPLICANT:  Merutka, Gene
;  APPLICANT:  Anwer, Mohmed
;  APPLICANT:  Lambert, Dennis
;  TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
;  TITLE OF INVENTION:  PHARMACOKINETIC PROPERTIES
;  FILE REFERENCE: 7872-043
;  CURRENT APPLICATION NUMBER: US/09/834,784
;  CURRENT FILING DATE:  2001-04-13
;  PRIOR APPLICATION NUMBER: 09/082,279
;  PRIOR FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 1515
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1480
;    LENGTH: 8
;    TYPE: PRT
;    ORGANISM: SIV
US-09-834-784-1480

  Query Match             46.2%;  Score 30;  DB 4;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 WMDISCWI 10
              | ||   |:
Db          1 WSDIWSWV 8


RESULT 14
US-08-431-539-11
; Sequence 11, Application US/08431539
; Patent No. 5580751
;  GENERAL INFORMATION:
;    APPLICANT:  Buchardt, Ole
;    APPLICANT:  Breddam, Klaus
;    APPLICANT:  Henriksen, Dennis
;    TITLE OF INVENTION:  Process for the Preparation of
;    TITLE OF INVENTION:  C-Terminally Amidated Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant & Gould
;      STREET:  3100 No. 5580751west Center
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/431,539
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/039,306
;      FILING DATE:  15-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nelson, Albin J.
;      REGISTRATION NUMBER:  28,650
;      REFERENCE/DOCKET NUMBER:  9663.8-US-WO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612-332-5300
;      TELEFAX:  612-332-9081
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-431-539-11

  Query Match             44.6%;  Score 29;  DB 1;  Length 6;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
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Db          1 YGWMD 5


RESULT 15
US-08-431-539-15
; Sequence 15, Application US/08431539
; Patent No. 5580751
;  GENERAL INFORMATION:
;    APPLICANT:  Buchardt, Ole
;    APPLICANT:  Breddam, Klaus
```

; APPLICANT: Henriksen, Dennis
; TITLE OF INVENTION: Process for the Preparation of
; TITLE OF INVENTION: C-Terminally Amidated Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5580751west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,539
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,306
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-431-539-15

Query Match 44.6%; Score 29; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 YSWMD 5
              | |||
Db          1 YGWMD 5
```

Search completed: August 4, 2003, 12:18:47
Job time : 29 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:12:50 ; Search time 38 Seconds
(without alignments)
25.308 Million cell updates/sec

Title: US-09-103-808-1
Perfect score: 65
Sequence: 1 YSWMDISCWI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	41.5	7	2	S33244	neuromodulatory pe
2	27	41.5	7	2	S33245	neuromodulatory pe
3	25	38.5	7	2	S33246	neuromodulatory pe
4	23	35.4	9	2	C57444	neuropeptide Grb-A
5	23	35.4	9	2	PT0272	Ig heavy chain CRD
6	22	33.8	5	2	A32516	cholecystokinin-5
7	22	33.8	8	2	PQ0012	cholecystokinin -
8	22	33.8	8	2	A43001	cholecystokinin -
9	22	33.8	8	2	JS0318	leucokinin VIII -
10	22	33.8	9	2	A61357	phyllocaerulein -
11	22	33.8	10	2	A61337	caerulein - frog (
12	22	33.8	10	2	A13687	caerulein-like pep
13	22	33.8	10	2	A59272	peptide-N4-(N-acet
14	22	33.8	10	2	PT0322	Ig heavy chain CRD
15	21.5	33.1	9	1	AKLQIM	locustamyoinhibiti
16	21	32.3	6	2	PD0028	pev-kinin 2 - pena
17	20	30.8	9	2	A57444	neuropeptide Grb-A
18	20	30.8	10	2	JC1367	thyroliberin poten
19	20	30.8	10	2	A21114	gonadoliberin - ch
20	20	30.8	10	2	T17054	cytochrome-c oxida
21	20	30.8	10	2	T17063	cytochrome-c oxida
22	19	29.2	9	2	B57444	neuropeptide Grb-A
23	19	29.2	10	2	PT0245	Ig heavy chain CRD
24	19	29.2	10	2	T14215	cytochrome-c oxida
25	19	29.2	10	2	T14223	cytochrome-c oxida
26	18	27.7	6	2	B34835	dnaA protein - Pse
27	18	27.7	9	2	PT0270	Ig heavy chain CRD
28	18	27.7	10	2	T17057	cytochrome-c oxida
29	18	27.7	10	2	T12303	cytochrome-c oxida
30	18	27.7	10	2	T17060	cytochrome-c oxida
31	18	27.7	10	2	T12308	cytochrome-c oxida
32	18	27.7	10	2	T17072	cytochrome-c oxida
33	18	27.7	10	2	T12316	cytochrome-c oxida
34	18	27.7	10	2	T12321	cytochrome-c oxida
35	17	26.2	6	2	A31263	dihydrofolate redu
36	17	26.2	6	2	B35640	cerebellar degener
37	17	26.2	7	2	S09652	hypothetical prote
38	17	26.2	8	2	C61512	variant surface gl
39	17	26.2	8	2	JS0316	leucokinin VI - Ma
40	17	26.2	10	2	T13976	cytochrome-c oxida
41	17	26.2	10	2	T12325	cytochrome-c oxida
42	17	26.2	10	2	T14043	cytochrome-c oxida
43	17	26.2	10	2	T14054	cytochrome-c oxida
44	17	26.2	10	2	T12329	cytochrome-c oxida
45	16	24.6	7	2	A61081	tryptophyllin, bas

ALIGNMENTS

RESULT 1
S33244
neuromodulatory peptide WWamide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33244
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia c
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33244
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 41.5%; Score 27; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 WMDISCW 9
              | ::| |
Db          1 WKEMSVW 7
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RESULT 2
S33245
neuromodulatory peptide WWamide-2 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33245
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33245
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 41.5%; Score 27; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 WMDISCW 9
              | ::| |
Db          1 WREMSVW 7
```

RESULT 3
S33246
neuromodulatory peptide WWamide-3 - giant African snail
C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33246
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33246
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 38.5%; Score 25; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| :| |
Db 1 WKQMSVW 7

RESULT 4
C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: C57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 35.4%; Score 23; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SWMDIS 7
:| |:|
Db 1 AWRDLS 6

RESULT 5
PT0272
Ig heavy chain CRD3 region (clone 3-103B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0272
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0272
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 35.4%; Score 23; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
|:| |
Db 1 YNWND 5

RESULT 6
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.8%; Score 22; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WMD 5
|||
Db 2 WMD 4

RESULT 7
PQ0012
cholecystokinin - southeastern quoll
N;Alternate names: CCK
C;Species: Dasyurus viverrinus (southeastern quoll)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C;Accession: PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: PQ0012
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.8%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WMD 5
|||
Db 5 WMD 7

RESULT 8
A43001
cholecystokinin - tammar wallaby
N;Alternate names: CCK
C;Species: Macropus eugenii (tammar wallaby)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C;Accession: A43001; PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: A43001
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 33.8%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 WMD 5
              |||
Db          5 WMD 7
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RESULT 9
JS0318
leucokinin VIII - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: JS0318
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir
A;Reference number: JS0317
A;Accession: JS0318
A;Molecule type: protein
A;Residues: 1-8 <HOL>
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 33.8%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 YSW 3
              |||
Db          5 YSW 7
```

RESULT 10
A61357
phyllocaerulein - Sauvage's leaf frog
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: A61357
R;Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
Br. J. Pharmacol. 37, 198-206, 1969
A;Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nona
A;Reference number: A61357; MUID:70005484; PMID:5824931
A;Accession: A61357
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ANA>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Binding site: sulfate (Tyr) (covalent) #status experimental
F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.8%; Score 22; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 WMD 5
              |||
Db          6 WMD 8
```

RESULT 11
A61337
caerulein - frog (Hyla caerulea)
C;Species: Hyla caerulea
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C;Accession: A61337
R;Anastasi, A.; Erspamer, V.; Endean, R.
Arch. Biochem. Biophys. 125, 57-68, 1968
A;Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the s
A;Reference number: A61337; MUID:68238534; PMID:5649531
A;Accession: A61337
A;Molecule type: protein
A;Residues: 1-10 <ANA>
C;Comment: The last five amino acids and the carboxyl terminal amide group of this n
C;Comment: This amphibian skin peptide can cause a sustained lowering of blood press
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.8%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 WMD 5
              |||
Db          7 WMD 9
```

RESULT 12
A13687
caerulein-like peptide - African tree frog (Kassina maculata)
C;Species: Kassina maculata
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 02-Sep-2000
C;Accession: A13687
R;Montecucchi, P.; Falconieri Erspamer, G.; Visser, J.
Experientia 33, 1138-1139, 1977
A;Title: Occurrence of Asn(2),Leu(5)-caerulein in the skin of the African frog Hylamb
A;Reference number: A13687; MUID:77246547; PMID:891852
A;Accession: A13687
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <MON>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotei
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;4/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 33.8%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.6e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          3 WMD 5
              |||
Db          7 WMD 9
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RESULT 13
A59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, large chai
N;Alternate names: peptide N-glycosidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 19-May-2000
C;Accession: A59272
R;Altmann, F.; Paschinger, K.; Dalik, T.; Vorauer, K.
Eur. J. Biochem. 252, 118-123, 1998
A;Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidas
A;Reference number: A59272; MUID:98181894; PMID:9523720
A;Accession: A59272
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <ALT>
C;Keywords: hydrolase

Query Match 33.8%; Score 22; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 YSWMD 5
              :|| |
Db          6 HSWAD 10
```

RESULT 14
PT0322
Ig heavy chain CRD3 region (clone J2-106A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0322
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0322
A;Molecule type: DNA
A;Residues: 1-10 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 33.8%; Score 22; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SWMDI 6
              ||| :
Db          6 SWMGV 10
```

RESULT 15
AKLQIM
locustamyoinhibiting peptide - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C;Accession: A60065
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Regul. Pept. 36, 111-119, 1991
A;Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI
A;Reference number: A60065; MUID:92179466; PMID:1796179
A;Accession: A60065
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and c
C;Superfamily: locustamyoinhibiting peptide
C;Keywords: amidated carboxyl end; hormone
F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.1%; Score 21.5; DB 1; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

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Qy          2 SWMDISC-W 9
              :| |::  |
Db          1 AWQDLNAGW 9
```

Search completed: August 4, 2003, 12:18:12
Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:06:05 ; Search time 24 Seconds
(without alignments)
19.594 Million cell updates/sec

Title: US-09-103-808-1
Perfect score: 65
Sequence: 1 YSWMDISCWI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 372

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	41.5	7	1	WWA1_ACHFU	P35919 achatina fu
2	27	41.5	7	1	WWA3_ACHFU	P35921 achatina fu
3	25	38.5	7	1	WWA2_ACHFU	P35920 achatina fu
4	24.5	37.7	9	1	PTSP_BOMMO	P82003 bombyx mori
5	22	33.8	8	1	CCKN_MACEU	P30369 macropus eu
6	22	33.8	8	1	LCK8_LEUMA	P19990 leucophaea
7	22	33.8	10	1	CAER_LITXA	P56264 litoria xan
8	21.5	33.1	9	1	LMIP_LOCMI	P31799 locusta mig
9	20	30.8	10	1	GON3_ONCKE	P20367 oncorhynchu
10	17	26.2	8	1	LCK4_LEUMA	P21143 leucophaea
11	17	26.2	8	1	LCK6_LEUMA	P19988 leucophaea
12	17	26.2	10	1	CA12_LITCI	P82086 litoria cit
13	16	24.6	6	1	EI01_LITRU	P82096 litoria rub
14	16	24.6	10	1	GON1_CHEPR	P80677 chelyosoma
15	15	23.1	4	1	OCP3_OCTMI	P58649 octopus min
16	15	23.1	5	1	UF01_MOUSE	P38639 mus musculu
17	15	23.1	6	1	LOK1_LOCMI	P41491 locusta mig
18	15	23.1	8	1	AKH_LIBAU	P25418 libellula a
19	15	23.1	8	1	LCK1_LEUMA	P21140 leucophaea
20	15	23.1	8	1	LCK2_LEUMA	P21141 leucophaea
21	15	23.1	8	1	LCK3_LEUMA	P21142 leucophaea
22	15	23.1	8	1	LCK5_LEUMA	P19987 leucophaea
23	15	23.1	8	1	LCK7_LEUMA	P19989 leucophaea
24	15	23.1	9	1	ISOT_CYPCA	P42993 cyprinus ca
25	15	23.1	9	1	OXYA_SCYCA	P42996 scyliorhinu
26	15	23.1	9	1	OXYA_SQUAC	P42999 squalus aca
27	15	23.1	9	1	OXYT_BUFRE	P42995 bufo regula
28	15	23.1	9	1	OXYT_CYPCA	P23879 cyprinus ca
29	15	23.1	9	1	OXYT_RABIT	P32878 oryctolagus
30	15	23.1	9	1	OXYT_RAJCL	P42994 raja clavat
31	15	23.1	9	1	OXYV_SQUAC	P43000 squalus aca
32	15	23.1	10	1	GONL_SQUAC	P27429 squalus aca
33	14	21.5	7	1	TPFY_PACDA	P83455 pachymedusa
34	14	21.5	8	1	ACI_THUAL	P18691 thunnus alb
35	14	21.5	9	1	CONO_CONGE	P05486 conus geogr
36	14	21.5	10	1	AEGL_AGRAE	P83465 agrocybe ae
37	13	20.0	8	1	AL16_CARMA	P81819 carcinus ma
38	13	20.0	9	1	D1_NEPNO	P24816 nephrops no
39	13	20.0	9	1	OXYT_EISFO	P42998 eisenia foe
40	13	20.0	10	1	GON2_CHICK	P37043 gallus gall
41	13	20.0	10	1	GON3_PETMA	P30948 petromyzon
42	13	20.0	10	1	MP2_MICOC	P81533 microplitis
43	12	18.5	5	1	AL14_CARMA	P81817 carcinus ma
44	12	18.5	7	1	BRHP_CONIM	P58803 conus imper
45	12	18.5	8	1	AL15_CARMA	P81818 carcinus ma

ALIGNMENTS

RESULT 1
WWA1_ACHFU
ID WWA1_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WWamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 41.5%; Score 27; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.3e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| ::| |
Db 1 WREMSVW 7

RESULT 2
WWA3_ACHFU
ID WWA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WWamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).

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DR   PIR; S33244; S33244.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  965 MW;  7362D5B69B132310 CRC64;

  Query Match             41.5%;  Score 27;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ::| |
Db          1 WKEMSVW 7


RESULT 3
WWA2_ACHFU
ID   WWA2_ACHFU     STANDARD;      PRT;      7 AA.
AC   P35920;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-1994 (Rel. 30, Last annotation update)
DE   WWamide-2.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX   NCBI_TaxID=6530;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Ganglion;
RX   MEDLINE=93265912; PubMed=8495720;
RA   Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT   "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT   ganglia of the African giant snail, Achatina fulica.";
RL   FEBS Lett. 323:104-108(1993).
DR   PIR; S33246; S33246.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  964 MW;  7362D5B686D32310 CRC64;

  Query Match             38.5%;  Score 25;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              |  :| |
Db          1 WKQMSVW 7


RESULT 4
PTSP_BOMMO
ID   PTSP_BOMMO     STANDARD;      PRT;      9 AA.
AC   P82003;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prothoracicostatic peptide (Bom-PTSP).
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=C145 X N140; TISSUE=Brain;
RX   MEDLINE=20002634; PubMed=10531308;
RA   Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA   Kataoka H.;
RT   "Identification of a prothoracicostatic peptide in the larval brain of
RT   the silkworm, Bombyx mori.";
RL   J. Biol. Chem. 274:31169-31173(1999).
RN   [2]
RP   ERRATUM.
RA   Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA   Kataoka H.;
RL   J. Biol. Chem. 275:9892-9892(2000).
CC   -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
CC       gland.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
KW   Hormone; Amidation.
FT   MOD_RES       9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  1090 MW;  3878C5B4472AB6C3 CRC64;

  Query Match             37.7%;  Score 24.5;  DB 1;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 SWMDI-SCW 9
              :| |: | |
Db          1 AWQDLNSAW 9


RESULT 5
CCKN_MACEU
ID   CCKN_MACEU     STANDARD;      PRT;      8 AA.
AC   P30369;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Cholecystokinin (CCK).
GN   CCK.
OS   Macropus eugenii (Tammar wallaby), and
OS   Dasyurus viverrinus (Southeastern quoll).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315, 9279;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=M.eugenii, and D.viverrinus;
RC   TISSUE=Brain;
RX   MEDLINE=88234141; PubMed=3375140;
RA   Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT   "Cholecystokinin octapeptide purified from brains of Australian
RT   marsupials.";
RL   Peptides 9:429-431(1988).
CC   -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC       AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC       IN THE BRAIN IS NOT CLEAR.
CC   -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR   PIR; A43001; A43001.
DR   PIR; PQ0012; PQ0012.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; 1.
KW   Amidation; Sulfation; Hormone.
FT   MOD_RES       2       2       SULFATION.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  1064 MW;  DDCAA68378768B5A CRC64;

  Query Match             33.8%;  Score 22;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WMD 5
              |||
Db          5 WMD 7


RESULT 6
LCK8_LEUMA
ID   LCK8_LEUMA     STANDARD;      PRT;      8 AA.
AC   P19990;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   Leucokinin VIII (L-VIII).
OS   Leucophaea maderae (Madeira cockroach).
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OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure and synthesis of leucokinins VII and
RT   VIII: the final members of this new family of cephalomyotropic
RT   peptides isolated from head extracts of Leucophaea maderae.";
RL   Comp. Biochem. Physiol. 88C:31-34(1987).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR   PIR; JS0318; JS0318.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  902 MW;  736365AB59CAADD8 CRC64;

  Query Match             33.8%;  Score 22;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              |||
Db          5 YSW 7


RESULT 7
CAER_LITXA
ID   CAER_LITXA     STANDARD;      PRT;     10 AA.
AC   P56264;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Caerulein.
OS   Litoria xanthomera (Orange-thighed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=79697;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97374000; PubMed=9230483;
RA   Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
RA   Ramsay S.L.;
RT   "New caerin antibacterial peptides from the skin glands of the
RT   Australian tree frog Litoria xanthomera.";
RL   J. Pept. Sci. 3:181-185(1997).
CC   -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC   -!- MASS SPECTROMETRY: MW=1354; METHOD=FAB.
CC   -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; 1.
KW   Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       4      4       SULFATION.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1290 MW;  99DBF3837861BB5A CRC64;

  Query Match             33.8%;  Score 22;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 3.9e+02;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WMD 5
              |||
Db          7 WMD 9


RESULT 8
LMIP_LOCMI
ID   LMIP_LOCMI     STANDARD;      PRT;     9 AA.
AC   P31799;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-OCT-1993 (Rel. 27, Last annotation update)
DE   Locustamyoinhibiting peptide (LOM-MIP).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92179466; PubMed=1796179;
RA   Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT   "Isolation, identification and synthesis of locustamyoinhibiting
RT   peptide (LOM-MIP), a novel biologically active neuropeptide from
RT   Locusta migratoria.";
RL   Regul. Pept. 36:111-119(1991).
CC   -!- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
CC       OVIDUCT.
CC   -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
CC       IN THE SUBOESOPHAGEAL GANGLION.
DR   PIR; A60065; AKLQIM.
KW   Amidation; Neuropeptide.
FT   MOD_RES       9      9       AMIDATION.
SQ   SEQUENCE   9 AA;  1060 MW;  387D7DD4472AB6C3 CRC64;

  Query Match             33.1%;  Score 21.5;  DB 1;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 SWMDISC-W 9
              :| |::  |
Db          1 AWQDLNAGW 9


RESULT 9
GON3_ONCKE
ID   GON3_ONCKE     STANDARD;      PRT;     10 AA.
AC   P20367; P81751;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Gonadoliberin III (Gonadotropin-releasing hormone III) (GnRH-III) (LH-
DE   RH III) (Luliberin III).
GN   GNRH3.
OS   Oncorhynchus keta (Chum salmon), and
OS   Clupea pallasii (Pacific herring).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8018, 30724;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=O.keta;
RX   MEDLINE=83195140; PubMed=6341999;
RA   Sherwood N., Eiden L., Brownstein M., Spiess J., Rivier J., Vale W.;
RT   "Characterization of a teleost gonadotropin-releasing hormone.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:2794-2798(1983).
RN   [2]
RP   SEQUENCE, AND FUNCTION.
RC   SPECIES=C.pallasii; TISSUE=Brain, and Pituitary;
RX   MEDLINE=20114351; PubMed=10650929;
RA   Carolsfeld J., Powell J.F.F., Park M., Fischer W.H., Craig A.G.,
RA   Chang J.P., Rivier J.E., Sherwood N.M.;
RT   "Primary structure and function of three gonadotropin-releasing
RT   hormones, including a novel form, from an ancient teleost, herring.";
RL   Endocrinology 141:505-512(2000).
CC   -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
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CC       the secretion of both luteinizing and follicle-stimulating
CC       hormones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GNRH family.
DR   PIR; A21114; A21114.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1230 MW;  284B3233786B45A3 CRC64;

  Query Match             30.8%;  Score 20;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 8.2e+02;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWM 4
              | |:
Db          5 YGWL 8


RESULT 10
LCK4_LEUMA
ID   LCK4_LEUMA     STANDARD;      PRT;      8 AA.
AC   P21143;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-MAY-1991 (Rel. 18, Last annotation update)
DE   Leucokinin IV (L-IV).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Primary structure and synthesis of two additional neuropeptides
RT   from Leucophaea maderae: members of a new family of
RT   Cephalomyotropins.";
RL   Comp. Biochem. Physiol. 84C:271-276(1986).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  906 MW;  DC6365B1E9D5BDDA CRC64;

  Query Match             26.2%;  Score 17;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              :||
Db          5 HSW 7


RESULT 11
LCK6_LEUMA
ID   LCK6_LEUMA     STANDARD;      PRT;      8 AA.
AC   P19988;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Leucokinin VI (L-VI).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RX   MEDLINE=87052651; PubMed=2877794;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure, and synthesis of leucokinins V and VI:
RT   myotropic peptides of Leucophaea maderae.";
RL   Comp. Biochem. Physiol. 88C:27-30(1987).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC       HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR   PIR; JS0316; JS0316.
KW   Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  935 MW;  9D6365B1E9D5A5A6 CRC64;

  Query Match             26.2%;  Score 17;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              :||
Db          5 HSW 7


RESULT 12
CA12_LITCI
ID   CA12_LITCI     STANDARD;      PRT;     10 AA.
AC   P82086;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Caerulein 1.2/1.2Y4.
OS   Litoria citropa (Australian blue mountains tree frog), and
OS   Litoria splendida (Magnificent tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=94770, 30345;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY (CAERULEINS 1.2 AND 1.2Y4).
RC   SPECIES=L.citropa; TISSUE=Skin secretion;
RX   MEDLINE=20057701; PubMed=10589099;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT   "Caerulein-like peptides from the skin glands of the Australian blue
RT   montains tree frog Litoria citropa. Part 1. Sequence determination
RT   using electrospray mass spectrometry.";
RL   Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
RN   [2]
RP   SEQUENCE, AND MASS SPECTROMETRY (CAERULEIN 1.2).
RC   SPECIES=L.splendida; TISSUE=Skin secretion;
RX   MEDLINE=20069371; PubMed=10601876;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C., Smith B.P.;
RT   "Differences in the skin peptides of the male and female Australian
RT   tree frog Litoria splendida. The discovery of the aquatic male sex
RT   pheromone splendipherin, together with Phe8 caerulein and the
RT   antibiotic peptide caerin 1.10.";
RL   Eur. J. Biochem. 267:269-275(2000).
CC   -!- FUNCTION: HYPOTENSIVE NEUROPEPTIDE (PROBABLE).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin dorsal glands.
CC   -!- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being
CC       sulfated.
CC   -!- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray.
CC   -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; FALSE_NEG.
KW   Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       4      4       SULFATION.
FT   MOD_RES      10     10       AMIDATION.
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SQ   SEQUENCE   10 AA;  1306 MW;  99DBFCD37861BB5A CRC64;

  Query Match             26.2%;  Score 17;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+03;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 WMD 5
              | |
Db          7 WFD 9


RESULT 13
EI01_LITRU
ID   EI01_LITRU     STANDARD;      PRT;      6 AA.
AC   P82096;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Electrin 1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
KW   Amphibian defense peptide; Amidation.
FT   MOD_RES       6      6       AMIDATION.
SQ   SEQUENCE   6 AA;  792 MW;  6683704772C9A000 CRC64;

  Query Match             24.6%;  Score 16;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WM 4
              ||
Db          5 WM 6


RESULT 14
GON1_CHEPR
ID   GON1_CHEPR     STANDARD;      PRT;     10 AA.
AC   P80677;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Gonadoliberin I (Gonadotropin-releasing hormone I) (GnRH-I)
DE   (Luliberin I).
OS   Chelyosoma productum.
OC   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
OC   Phlebobranchia; Corellidae; Chelyosoma.
OX   NCBI_TaxID=71177;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=96413669; PubMed=8816823;
RA   Powell J.F.F., Reska-Skinner S.M., Prakash M.O., Fischer W.H.,
RA   Park M., Rivier J.E., Craig A.G., Mackie G.O., Sherwood N.M.;
RT   "Two new forms of gonadotropin-releasing hormone in a protochordate
RT   and the evolutionary implications.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464(1996).
CC   -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC       the secretion of both luteinizing and follicle-stimulating
CC       hormones.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: GNRH NEURONS LIE WITHIN BLOOD SINUSES CLOSE TO
CC       THE GONODUCTS AND GONADS IN BOTH JUVENILES AND ADULTS, IMPLYING
CC       THAT THE NEUROPEPTIDE IS RELEASED INTO THE BLOODSTREAM.
CC   -!- MASS SPECTROMETRY: MW=1246.56; METHOD=MALDI.
CC   -!- SIMILARITY: Belongs to the GNRH family.
DR   InterPro; IPR002012; GnRH.
DR   Pfam; PF00446; GnRH; 1.
DR   PROSITE; PS00473; GNRH; 1.
KW   Hormone; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION (BY SIMILARITY).
SQ   SEQUENCE   10 AA;  1264 MW;  284B3639DB5AB5A3 CRC64;

  Query Match             24.6%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   66.7%;  Pred. No. 3.6e+03;
  Matches    2;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 WMD 5
              | |
Db          3 WSD 5


RESULT 15
OCP3_OCTMI
ID   OCP3_OCTMI     STANDARD;      PRT;      4 AA.
AC   P58649;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cardioactive peptides Ocp-3/Ocp-4.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-4 is a 1000 time less
CC       active than Ocp-3.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES       2      2       D-SERINE (IN OCP-4).
SQ   SEQUENCE   4 AA;  463 MW;  6AB365B810000000 CRC64;

  Query Match             23.1%;  Score 15;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SW 3
              ||
Db          2 SW 3


Search completed: August  4, 2003, 12:15:46
Job time : 26 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:12:30 ; Search time 93 Seconds
(without alignments)
27.748 Million cell updates/sec

Title: US-09-103-808-1
Perfect score: 65
Sequence: 1 YSWMDISCWI 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1349

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	22	33.8	10	10	Q99213	Q99213 aegilops sq
2	22	33.8	10	10	P81899	P81899 prunus dulc
3	22	33.8	10	13	Q9PRU9	Q9pru9 sparus aura
4	21	32.3	8	11	O35835	O35835 rattus sp.
5	20	30.8	8	4	Q15888	Q15888 homo sapien
6	20	30.8	8	6	Q9TRY3	Q9try3 sus sp. ins
7	20	30.8	10	8	Q9T8P3	Q9t8p3 liolaemus a
8	20	30.8	10	8	Q9T8L9	Q9t8l9 liolaemus f
9	20	30.8	10	8	Q9T8W5	Q9t8w5 liolaemus r
10	20	30.8	10	8	Q8W916	Q8w916 liolaemus m
11	20	30.8	10	8	Q9T8N7	Q9t8n7 liolaemus o
12	20	30.8	10	8	O79897	O79897 hoplocercus
13	20	30.8	10	8	O79888	O79888 basiliscus
14	20	30.8	10	8	Q9T8P0	Q9t8p0 liolaemus f
15	20	30.8	10	8	Q9TFV5	Q9tfv5 eublepharus
16	19	29.2	8	8	Q9T4Y2	Q9t4y2 asterina pe
17	19	29.2	9	2	Q8GL31	Q8gl31 borrelia bu
18	19	29.2	9	2	Q8GL26	Q8gl26 borrelia bu
19	19	29.2	9	4	Q16386	Q16386 homo sapien
20	19	29.2	10	8	Q9TG83	Q9tg83 diploglossu
21	19	29.2	10	8	Q8SIU4	Q8siu4 xantusia he
22	19	29.2	10	8	P92766	P92766 varanus gri
23	19	29.2	10	8	Q9TGA1	Q9tga1 heloderma s
24	19	29.2	10	8	Q8SIT8	Q8sit8 xantusia ar
25	19	29.2	10	8	Q9TG44	Q9tg44 anguis frag
26	19	29.2	10	8	Q9TG92	Q9tg92 anniella pu
27	19	29.2	10	8	Q9TG74	Q9tg74 wetmorena h
28	19	29.2	10	8	Q9TG77	Q9tg77 sauresia ag
29	19	29.2	10	8	P92774	P92774 xantusia vi
30	19	29.2	10	8	Q8SIU1	Q8siu1 xantusia be
31	18	27.7	10	2	Q47475	Q47475 escherichia
32	18	27.7	10	8	Q9T8K7	Q9t8k7 liolaemus m
33	18	27.7	10	8	Q9T8N1	Q9t8n1 liolaemus p
34	18	27.7	10	8	Q9T8T6	Q9t8t6 liolaemus m
35	18	27.7	10	8	Q9T8L3	Q9t8l3 liolaemus l
36	18	27.7	10	8	Q9T8G8	Q9t8g8 liolaemus c
37	18	27.7	10	8	Q9T8X7	Q9t8x7 phymaturus
38	18	27.7	10	8	Q9T8Q5	Q9t8q5 liolaemus l
39	18	27.7	10	8	Q9T8L0	Q9t8l0 liolaemus o
40	18	27.7	10	8	Q9T8W8	Q9t8w8 liolaemus b
41	18	27.7	10	8	Q9T8R4	Q9t8r4 liolaemus p
42	18	27.7	10	8	Q9T8M8	Q9t8m8 liolaemus m
43	18	27.7	10	8	Q9T8S1	Q9t8s1 liolaemus l
44	18	27.7	10	8	Q9T8S4	Q9t8s4 liolaemus c
45	18	27.7	10	8	Q9T8T9	Q9t8t9 liolaemus l

ALIGNMENTS

RESULT 1
Q99213
ID Q99213 PRELIMINARY; PRT; 10 AA.
AC Q99213;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Albumin (Fragment).
OS Aegilops squarrosa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP SEQUENCE.
RA Shewry P.R., Lafiandra D., Salcedo G., Aragoncillo C.,
RA Garcia-Olmedo F., Lew E.J.-L., Dietler M.D., Kasarda D.D.;
RL FEBS Lett. 175:359-363(1984).
KW Seed storage protein.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1105 MW; 3A1AB5AEA365A367 CRC64;

Query Match 33.8%; Score 22; DB 10; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
:|| |
Db 4 WSWCD 8

RESULT 2
P81899
ID P81899 PRELIMINARY; PRT; 10 AA.
AC P81899;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A, large

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DE   chain (Subunit A) (EC 3.5.1.52) (PNGase A) (Glycopeptide N-
DE   glycosidase) (N-glycanase) (Fragment).
OS   Prunus dulcis (Almond) (Prunus amygdalus).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX   NCBI_TaxID=3755;
RN   [1]
RP   SEQUENCE, AND CHARACTERIZATION.
RX   PubMed=9523720;
RA   Altmann F., Paschinger K., Dalik T., Vorauer K.;
RT   "Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine
RT   amidase A and its N-glycans.";
RL   Eur. J. Biochem. 252:118-123(1998).
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF AN N4-(ACETYL-BETA-D-
CC       GLUCOSAMINYL)ASPARAGINE RESIDUE IN WHICH THE N-ACETYL-D-
CC       GLUCOSAMINE RESIDUE MAY BE FURTHER GLYCOSYLATED, TO YIELD A
CC       (SUBSTITUTED) N-ACETYL-BETA-D-GLUCOSAMINYLAMINE AND THE PEPTIDE
CC       CONTAINING AN ASPARTIC RESIDUE.
CC   -!- SUBUNIT: HETERODIMER OF A LARGE AND A SMALL CHAIN.
CC   -!- PTM: IS HIGHLY GLYCOSYLATED AND IS RESISTANT AGAINST SELF-
CC       DEGLYCOSYLATION.
CC   -!- MASS SPECTROMETRY: MW=54182; METHOD=MALDI.
KW   Hydrolase; Glycoprotein.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1106 MW;  95F6BF65B1FB5865 CRC64;

  Query Match             33.8%;  Score 22;  DB 10;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 2.4e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
              :|| |
Db          6 HSWAD 10


RESULT 3
Q9PRU9
ID   Q9PRU9      PRELIMINARY;      PRT;    10 AA.
AC   Q9PRU9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Gonadotropin-releasing hormone, SBGNRH-I.
OS   Sparus aurata (Gilthead sea bream).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sparidae; Sparus.
OX   NCBI_TaxID=8175;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=95083645; PubMed=7991588;
RA   Powell J.F., Zohar Y., Elizur A., Park M., Fischer W.H., Craig A.G.,
RA   Rivier J.E., Lovejoy D.A., Sherwood N.M.;
RT   "Three forms of gonadotropin-releasing hormone characterized from
RT   brains of one species.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).
SQ   SEQUENCE   10 AA;  1132 MW;  81566865AB587735 CRC64;

  Query Match             33.8%;  Score 22;  DB 13;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              |||
Db          6 YSW 8


RESULT 4
O35835
ID   O35835      PRELIMINARY;      PRT;     8 AA.
AC   O35835;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   ORF1 protein.
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=98008057; PubMed=9581555;
RA   Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT   "Human and rat testis express two mRNA species encoding varients of
RT   NRD convertase, a metalloendopeptidase of the insulinase family.";
RL   Biochem. J. 327:773-779(1997).
DR   EMBL; X93208; CAA63695.1; -.
SQ   SEQUENCE   8 AA;  886 MW;  EA7EA1B1ADC5A5B6 CRC64;

  Query Match             32.3%;  Score 21;  DB 11;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SCW 9
              :||
Db          6 TCW 8


RESULT 5
Q15888
ID   Q15888      PRELIMINARY;      PRT;     8 AA.
AC   Q15888;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (Clone XP15H8A) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32069; AAA73878.1; -.
FT   NON_TER      1      1
FT   NON_TER      8      8
SQ   SEQUENCE   8 AA;  1068 MW;  0315A37EAB5B0763 CRC64;

  Query Match             30.8%;  Score 20;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CW 9
              ||
Db          5 CW 6


RESULT 6
Q9TRY3
ID   Q9TRY3      PRELIMINARY;      PRT;     8 AA.
AC   Q9TRY3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS   Sus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9826;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92049376; PubMed=1719383;
RA   Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT   "Isolation and molecular cloning of insulin-like growth factor-binding
RT   protein-6.";
RL   Mol. Endocrinol. 5:938-948(1991).
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  850 MW;  9FB2CEA37EA7687D CRC64;

  Query Match             30.8%;  Score 20;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CW 9
              ||
Db          4 CW 5


RESULT 7
Q9T8P3
ID   Q9T8P3      PRELIMINARY;      PRT;    10 AA.
AC   Q9T8P3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Liolaemus andinus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=109394;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT   "Phylogenetic relationships in the iguanid lizard Genus Liolaemus:
RT   Multiple origins of viviparous reproduction and evidence for recurring
RT   Andean vicariance and dispersal.";
RL   Biol. J. Linn. Soc. 69:75-102(2000).
DR   EMBL; AF099245; AAF18841.1; -.
KW   Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 8
Q9T8L9
ID   Q9T8L9      PRELIMINARY;      PRT;    10 AA.
AC   Q9T8L9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Liolaemus fitzingerii.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=109412;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT   "Phylogenetic relationships in the iguanid lizard Genus Liolaemus:
RT   Multiple origins of viviparous reproduction and evidence for recurring
RT   Andean vicariance and dispersal.";
RL   Biol. J. Linn. Soc. 69:75-102(2000).
DR   EMBL; AF099253; AAF18865.1; -.
KW   Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 9
Q9T8W5
ID   Q9T8W5      PRELIMINARY;      PRT;    10 AA.
AC   Q9T8W5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Liolaemus robertmertensi.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=109435;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SDSU3498;
RA   Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT   "Phylogenetic relationships in the iguanid lizard Genus Liolaemus:
RT   Multiple origins of viviparous reproduction and evidence for recurring
RT   Andean vicariance and dispersal.";
RL   Biol. J. Linn. Soc. 69:75-102(2000).
DR   EMBL; AF099220; AAF18766.1; -.
KW   Mitochondrion.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 10
Q8W916
ID   Q8W916      PRELIMINARY;      PRT;    10 AA.
AC   Q8W916;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Liolaemus molinai.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=166936;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Valladares J.P., Etheridge R., Schulte J.A. II.;
RT   "Description of a new species of altiplanico lizard of the group
```

```
RT   montanus, Liolaemus molinai.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF305915; AAL55815.1; -.
DR   EMBL; AF305916; AAL55818.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 11
Q9T8N7
ID   Q9T8N7      PRELIMINARY;      PRT;    10 AA.
AC   Q9T8N7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Liolaemus orientalis.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=109468;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SDSU3517;
RA   Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT   "Phylogenetic relationships in the iguanid lizard Genus Liolaemus:
RT   Multiple origins of viviparous reproduction and evidence for recurring
RT   Andean vicariance and dispersal.";
RL   Biol. J. Linn. Soc. 69:75-102(2000).
DR   EMBL; AF099247; AAF18847.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 12
O79897
ID   O79897      PRELIMINARY;      PRT;    10 AA.
AC   O79897;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Hoplocercus spinosus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Hoplocercinae;
OC   Hoplocercus.
OX   NCBI_TaxID=52193;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97315309; PubMed=9169559;
RA   Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT   "Evolutionary shifts in three major structural features of the
RT   mitochondrial genome among iguanian lizards.";
RL   J. Mol. Evol. 44:660-674(1997).
DR   EMBL; U82683; AAC62284.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1288 MW;  0A3480C7336415B0 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 5.1e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              .| || |:
Db          1 MFISRWL 7


RESULT 13
O79888
ID   O79888      PRELIMINARY;      PRT;    10 AA.
AC   O79888;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Basiliscus plumifrons.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Corytophaninae;
OC   Basiliscus.
OX   NCBI_TaxID=52191;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97315309; PubMed=9169559;
RA   Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
RT   "Evolutionary shifts in three major structural features of the
RT   mitochondrial genome among iguanian lizards.";
RL   J. Mol. Evol. 44:660-674(1997).
DR   EMBL; U82680; AAC62269.1; -.
KW   Mitochondrion.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 14
Q9T8P0
ID   Q9T8P0      PRELIMINARY;      PRT;    10 AA.
AC   Q9T8P0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Liolaemus famatinae.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Iguania; Iguanidae; Tropidurinae; Liolaemus.
OX   NCBI_TaxID=109411;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Schulte J.A. II, Macey J.R., Espinoza R.E., Larson A.;
RT   "Phylogenetic relationships in the iguanid lizard Genus Liolaemus:
RT   Multiple origins of viviparous reproduction and evidence for recurring
RT   Andean vicariance and dispersal.";
RL   Biol. J. Linn. Soc. 69:75-102(2000).
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DR   EMBL; AF099246; AAF18844.1; -.
KW   Mitochondrion.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1254 MW;  1A3580C733640440 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | |: |:
Db          1 MSINRWL 7


RESULT 15
Q9TFV5
ID   Q9TFV5      PRELIMINARY;      PRT;    10 AA.
AC   Q9TFV5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Cytochrome c oxidase subunit I (Fragment).
GN   COI.
OS   Eublepharus turkmenicus.
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Gekkota; Eublepharidae;
OC   Eublepharus.
OX   NCBI_TaxID=52219;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99343618; PubMed=10413626;
RA   Macey J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
RT   "Vicariant patterns of fragmentation among gekkonid lizards of the
RT   genus teratoscincus produced by the indian collision: A molecular
RT   phylogenetic perspective and an area cladogram for central asia.";
RL   Mol. Phylogenet. Evol. 12:320-332(1999).
DR   EMBL; AF114248; AAD51596.1; -.
KW   Mitochondrion.
FT   NON_TER      10      10
SQ   SEQUENCE   10 AA;  1241 MW;  5DEE80C7336415B7 CRC64;

  Query Match             30.8%;  Score 20;  DB 8;  Length 10;
  Best Local Similarity   42.9%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCWI 10
              | :| |:
Db          1 MTLSRWL 7


Search completed: August  4, 2003, 12:17:28
Job time : 96 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:20:21 ; Search time 39 Seconds
(without alignments)
36.629 Million cell updates/sec

Title: US-09-103-808-2
Perfect score: 61
Sequence: 1 YSWMDISCW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 179625

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
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24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	9	18	AAW16577	Human gastric canc
2	31	50.8	9	22	AAB66551	Phage clone ed1 pI
3	30	49.2	8	22	ABP15183	HIV A24 super moti
4	30	49.2	8	22	ABP24036	HIV A24 motif env
5	30	49.2	9	22	ABP15292	HIV A24 super moti
6	30	49.2	9	22	ABP15394	HIV A24 super moti
7	30	49.2	9	22	ABP15485	HIV A24 super moti
8	30	49.2	9	22	ABP19698	HIV A01 motif env
9	30	49.2	9	22	ABP19896	HIV A03 motif env
10	30	49.2	9	22	ABP22345	HIV A11 motif env
11	30	49.2	9	22	ABP24037	HIV A24 motif env
12	30	49.2	9	22	ABP24040	HIV A24 motif env
13	29	47.5	5	5	AAP40008	Sequence of gastri
14	29	47.5	7	5	AAP40033	Sequence of gastri
15	29	47.5	7	6	AAP50373	Gastric acid secre
16	29	47.5	7	21	AAY51308	Human gastrin G17
17	29	47.5	8	6	AAP50374	Gastric acid secre
18	29	47.5	8	16	AAR79689	pp60(c-src) kinase
19	29	47.5	8	21	AAY57990	Gastrin peptide SE
20	29	47.5	9	16	AAR79712	EGF receptor Tyr k
21	29	47.5	9	21	AAY67913	Gastrin peptide SE
22	28	45.9	6	22	AAB49571	RT-loop peptide fr
23	27	44.3	7	14	AAR38734	WWamide 1. Achati
24	27	44.3	8	22	AAB78533	SIV gp 41 enhancer
25	27	44.3	8	23	ABJ06730	Hepatitis B virus
26	27	44.3	8	23	ABJ08663	Hepatitis B virus
27	27	44.3	9	15	AAR59139	Peptide fragment (
28	27	44.3	9	18	AAW13439	Brain homing pepti
29	27	44.3	9	20	AAY46033	Immunogenic peptid
30	27	44.3	9	20	AAY46441	Immunogenic peptid
31	27	44.3	9	20	AAY46498	Immunogenic peptid
32	27	44.3	9	21	AAM49132	Hepatitis B virus
33	27	44.3	9	21	AAB07399	Brain homing pepti
34	27	44.3	9	21	AAY73072	Hepatitis B virus
35	27	44.3	9	22	AAE11805	Phage peptide #13
36	27	44.3	9	22	AAB75910	Hepatitis B virus
37	27	44.3	9	23	ABJ06172	Hepatitis B virus
38	27	44.3	9	23	ABJ06710	Hepatitis B virus
39	27	44.3	9	23	ABJ06887	Hepatitis B virus
40	27	44.3	9	23	ABJ07567	Hepatitis B virus
41	27	44.3	9	23	ABJ08316	Hepatitis B virus
42	27	44.3	9	23	ABJ08712	Hepatitis B virus
43	27	44.3	9	23	ABJ08792	Hepatitis B virus
44	27	44.3	9	23	ABJ08822	Hepatitis B virus
45	27	44.3	9	23	ABJ08849	Hepatitis B virus

ALIGNMENTS

RESULT 1
AAW16577
ID AAW16577 standard; peptide; 9 AA.
XX
AC AAW16577;
XX
DT 27-JAN-1998 (first entry)
XX
DE Human gastric cancer antigen fragment 2.
XX
KW Gastric cancer; gastric cancer antigen; human leukocyte antigen;
KW HLA; cytotoxic T lymphocyte; CTL; recombinant bacterium;
KW recombinant virus; gastric cancer; vaccine.
XX
OS Homo sapiens.
XX
PN EP770624-A2.
XX
PD 02-MAY-1997.
XX
PF 30-SEP-1996; 96EP-0307163.
XX
PR 19-AUG-1996; 96JP-0217140.
PR 29-SEP-1995; 95JP-0253491.
XX
PA (AJIN) AJINOMOTO CO INC.
PA (KIKU/) KIKUCHI K.
XX
PI Hamuro J, Kikuchi K, Sahara H, Sato N, Suzuki M;
PI Wada Y, Yasojima T;
XX
DR WPI; 1997-238096/22.

XX
PT Gastric cancer antigen fragment present in human gastric cancer cell
PT - induces cytotoxic T lymphocyte response when bound to human
PT leukocyte antigen, for gastric cancer treatment or prevention
XX
PS Claim 5; Page 9; 14pp; English.
XX
CC This novel peptide is a fragment of a gastric cancer antigen present in
CC a human gastric cancer cell, which when bound to a human leukocyte
CC antigen (HLA), is capable of inducing a cytotoxic T lymphocyte (CTL)
CC response that targets the gastric cancer cell. It is based on amino acids
CC 1-9 of peptide 1 (AAW16576), whih shows the same effect. However,
CC peptides containing amino acids 1-8 and 1-7 of peptide 1 have no CTL
CC inducibility, and cannot be used. The HLA-bound peptides can be used to
CC treat or prevent gastric cancer. Viruses, e.g. vaccinia virus, or
CC bacteria, e.g. BCG, which contain the DNA encoding this peptide can be
CC used as a live vaccine for preventing or treating human gastric cancer.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 61; DB 18; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWMDISCW 9
|||||||||
Db 1 YSWMDISCW 9

RESULT 2
AAB66551
ID AAB66551 standard; peptide; 9 AA.
XX
AC AAB66551;
XX
DT 10-APR-2001 (first entry)
XX
DE Phage clone ed1 pIII-displayed peptide.
XX
KW phage display; antianaemic; cytostatic; immunosuppressive;
KW immunoglobulin M; IgM; IgM binding; autoimmune haemolytic anaemia;
KW paraneoplastic syndrome; multiple myeloma; cancer; autoimmune disease.
XX
OS Synthetic.
XX
PN WO200102001-A1.
XX
PD 11-JAN-2001.
XX
PF 03-JUL-2000; 2000WO-US18320.
XX
PR 02-JUL-1999; 99US-0142048.
PR 06-JUL-1999; 99US-0142389.
PR 07-JUL-1999; 99US-0142524.
XX
PA (RERE-) RES & DEV INST INC.
XX
PI Glee PM, Pincus SH, Burritt JB, Cutler JE;
XX
DR WPI; 2001-138063/14.
XX
PT Novel peptides that bind to immunoglobulin M antibodies and block their
PT interaction with antigens, useful for treating rheumatoid factor biding
PT to immunoglobulin G, autoimmune hemolytic anemia or paraneoplastic
PT syndromes -
XX
PS Claim 10; Page 6; 60pp; English.
XX
CC The present sequence is one of a number of random 9-mer peptides which
CC were displayed from the N-terminal portion of the pIII capsid protein of
CC filamentous bacteriophage M13KBst. Peptides that selectively bind to
CC immunoglobulin (Ig)M antibodies but do not selectively bind to antibodies
CC of other classes were identified. Such peptides are useful for detecting
CC the presence of IgM in a sample and for purifying IgM from a sample.
CC The peptides are also useful for isolating an antigen specific IgM
CC population or for isolating an antigen bound by a specific IgM
CC population. They are useful for treating a human disease associated with
CC IgM antibodies such as rheumatoid factor binding to IgG,
CC isohaemagglutinin binding to red blood cells, autoimmune haemolytic
CC anaemia, paranecplastic syndromes, multiple myeloma or cancer.
CC The peptides are useful for treating diseases such as cancer or an
CC autoimmune disease associated with IgM antibodies by removing IgM from
CC serum. The peptides are capable of selectively binding to the IgM
CC molecules of several mammalian species and to both the pentameric and
CC monomeric forms of IgM molecules.
XX
SQ Sequence 9 AA;

Query Match 50.8%; Score 31; DB 22; Length 9;
Best Local Similarity 44.4%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YSWMDISCW 9
| |: | |
Db 1 YDWIPSSAW 9

RESULT 3
ABP15183
ID ABP15183 standard; Peptide; 8 AA.
XX
AC ABP15183;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #63.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 180; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present

CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 22; Length 8;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| ||: |
Db 1 WFDITNW 7

RESULT 4
ABP24036
ID ABP24036 standard; Peptide; 8 AA.
XX
AC ABP24036;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 motif env peptide #2.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 362; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 22; Length 8;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| ||: |
Db 1 WFDITNW 7

RESULT 5
ABP15292
ID ABP15292 standard; Peptide; 9 AA.
XX
AC ABP15292;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #172.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 182; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response

CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 30; DB 22; Length 9;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| ||: |
Db 1 WFDITNW 7

RESULT 6
ABP15394
ID ABP15394 standard; Peptide; 9 AA.
XX
AC ABP15394;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #274.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 184; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 30; DB 22; Length 9;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| ||: |
Db 1 WFDITNW 7

RESULT 7
ABP15485
ID ABP15485 standard; Peptide; 9 AA.
XX
AC ABP15485;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 super motif env peptide #365.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 186; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

```
  Query Match             49.2%;  Score 30;  DB 22;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ||: |
Db          1 WFDITNW 7
```

```
RESULT 8
ABP19698
ID   ABP19698 standard; Peptide; 9 AA.
XX
AC   ABP19698;
XX
DT   15-JUL-2002  (first entry)
XX
DE   HIV A01 motif env peptide #8.
XX
KW   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW   vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW   antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200124810-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US27766.
XX
PR   05-OCT-1999;   99US-0412863.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Sidney J,  Southwood S,  Livingston BD,  Chesnut R;
PI   Baker DM,  Celis E,  Kubo RT,  Grey HM;
XX
DR   WPI; 2001-354887/37.
XX
PT   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT   peptide groups, useful for vaccinating against HIV-1 -
XX
PS   Claim 32; Page 273; 448pp; English.
XX
CC   The present invention describes a composition (I) comprising a prepared
CC   human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC   sequence selected from 51 defined amino acid sequences (ABL25347 to
CC   ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC   may be used for immunising subjects against HIV-1 infections. The use of
CC   group-based vaccines has several advantages over traditional vaccines,
CC   particularly when compared to the use of whole antigens in vaccine
CC   compositions. There is evidence that the immune response to whole
CC   antigens is directed largely toward variable regions of the antigen,
CC   allowing for immune escape due to mutations. The groups for inclusion in
CC   an group-based vaccine may be selected from conserved regions of viral or
CC   tumour-associated antigens, which therefore reduces the likelihood of
CC   escape mutants. Furthermore, immunosuppressive groups that may be present
CC   in whole antigens can be avoided with the use of group-based vaccines.
CC   An additional advantage of an group-based vaccine approach is the ability
CC   to combine selected groups (CTL and HTL), and further, to modify the
CC   composition of the groups, achieving, for example, enhanced
CC   immunogenicity. Accordingly, the immune response can be modulated, as
CC   appropriate, for the target disease. Similar engineering of the response
CC   is not possible with traditional approaches. ABP11501 to ABP25412
CC   represent peptide sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   9 AA;
```

```
  Query Match             49.2%;  Score 30;  DB 22;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ||: |
Db          1 WFDITNW 7
```

```
RESULT 9
ABP19896
ID   ABP19896 standard; Peptide; 9 AA.
XX
AC   ABP19896;
XX
DT   15-JUL-2002  (first entry)
XX
DE   HIV A03 motif env peptide #100.
XX
KW   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW   vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW   antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200124810-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US27766.
XX
PR   05-OCT-1999;   99US-0412863.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Sidney J,  Southwood S,  Livingston BD,  Chesnut R;
PI   Baker DM,  Celis E,  Kubo RT,  Grey HM;
XX
DR   WPI; 2001-354887/37.
XX
PT   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT   peptide groups, useful for vaccinating against HIV-1 -
XX
PS   Claim 32; Page 277; 448pp; English.
XX
CC   The present invention describes a composition (I) comprising a prepared
CC   human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC   sequence selected from 51 defined amino acid sequences (ABL25347 to
CC   ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC   may be used for immunising subjects against HIV-1 infections. The use of
CC   group-based vaccines has several advantages over traditional vaccines,
CC   particularly when compared to the use of whole antigens in vaccine
CC   compositions. There is evidence that the immune response to whole
CC   antigens is directed largely toward variable regions of the antigen,
CC   allowing for immune escape due to mutations. The groups for inclusion in
CC   an group-based vaccine may be selected from conserved regions of viral or
CC   tumour-associated antigens, which therefore reduces the likelihood of
CC   escape mutants. Furthermore, immunosuppressive groups that may be present
CC   in whole antigens can be avoided with the use of group-based vaccines.
CC   An additional advantage of an group-based vaccine approach is the ability
CC   to combine selected groups (CTL and HTL), and further, to modify the
CC   composition of the groups, achieving, for example, enhanced
CC   immunogenicity. Accordingly, the immune response can be modulated, as
CC   appropriate, for the target disease. Similar engineering of the response
CC   is not possible with traditional approaches. ABP11501 to ABP25412
CC   represent peptide sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   9 AA;
```

```
  Query Match             49.2%;  Score 30;  DB 22;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ||: |
```

```
Db          1 WFDITNW 7


RESULT 10
ABP22345
ID   ABP22345 standard; Peptide; 9 AA.
XX
AC   ABP22345;
XX
DT   15-JUL-2002  (first entry)
XX
DE   HIV A11 motif env peptide #68.
XX
KW   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW   vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW   antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200124810-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US27766.
XX
PR   05-OCT-1999;   99US-0412863.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Sidney J,  Southwood S,  Livingston BD,  Chesnut R;
PI   Baker DM,  Celis E,  Kubo RT,  Grey HM;
XX
DR   WPI; 2001-354887/37.
XX
PT   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT   peptide groups, useful for vaccinating against HIV-1 -
XX
PS   Claim 32; Page 327; 448pp; English.
XX
CC   The present invention describes a composition (I) comprising a prepared
CC   human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC   sequence selected from 51 defined amino acid sequences (ABL25347 to
CC   ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC   may be used for immunising subjects against HIV-1 infections. The use of
CC   group-based vaccines has several advantages over traditional vaccines,
CC   particularly when compared to the use of whole antigens in vaccine
CC   compositions. There is evidence that the immune response to whole
CC   antigens is directed largely toward variable regions of the antigen,
CC   allowing for immune escape due to mutations. The groups for inclusion in
CC   an group-based vaccine may be selected from conserved regions of viral or
CC   tumour-associated antigens, which therefore reduces the likelihood of
CC   escape mutants. Furthermore, immunosuppressive groups that may be present
CC   in whole antigens can be avoided with the use of group-based vaccines.
CC   An additional advantage of an group-based vaccine approach is the ability
CC   to combine selected groups (CTL and HTL), and further, to modify the
CC   composition of the groups, achieving, for example, enhanced
CC   immunogenicity. Accordingly, the immune response can be modulated, as
CC   appropriate, for the target disease. Similar engineering of the response
CC   is not possible with traditional approaches. ABP11501 to ABP25412
CC   represent peptide sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   9 AA;

  Query Match             49.2%;  Score 30;  DB 22;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ||: |
Db          1 WFDITNW 7


RESULT 11
ABP24037
ID   ABP24037 standard; Peptide; 9 AA.
XX
AC   ABP24037;
XX
DT   15-JUL-2002  (first entry)
XX
DE   HIV A24 motif env peptide #3.
XX
KW   HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW   vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW   antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS   Human immunodeficiency virus type 1.
XX
PN   WO200124810-A1.
XX
PD   12-APR-2001.
XX
PF   05-OCT-2000; 2000WO-US27766.
XX
PR   05-OCT-1999;   99US-0412863.
XX
PA   (EPIM-) EPIMMUNE INC.
XX
PI   Sette A,  Sidney J,  Southwood S,  Livingston BD,  Chesnut R;
PI   Baker DM,  Celis E,  Kubo RT,  Grey HM;
XX
DR   WPI; 2001-354887/37.
XX
PT   Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT   peptide groups, useful for vaccinating against HIV-1 -
XX
PS   Claim 32; Page 362; 448pp; English.
XX
CC   The present invention describes a composition (I) comprising a prepared
CC   human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC   sequence selected from 51 defined amino acid sequences (ABL25347 to
CC   ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC   may be used for immunising subjects against HIV-1 infections. The use of
CC   group-based vaccines has several advantages over traditional vaccines,
CC   particularly when compared to the use of whole antigens in vaccine
CC   compositions. There is evidence that the immune response to whole
CC   antigens is directed largely toward variable regions of the antigen,
CC   allowing for immune escape due to mutations. The groups for inclusion in
CC   an group-based vaccine may be selected from conserved regions of viral or
CC   tumour-associated antigens, which therefore reduces the likelihood of
CC   escape mutants. Furthermore, immunosuppressive groups that may be present
CC   in whole antigens can be avoided with the use of group-based vaccines.
CC   An additional advantage of an group-based vaccine approach is the ability
CC   to combine selected groups (CTL and HTL), and further, to modify the
CC   composition of the groups, achieving, for example, enhanced
CC   immunogenicity. Accordingly, the immune response can be modulated, as
CC   appropriate, for the target disease. Similar engineering of the response
CC   is not possible with traditional approaches. ABP11501 to ABP25412
CC   represent peptide sequences used in the exemplification of the present
CC   invention.
XX
SQ   Sequence   9 AA;

  Query Match             49.2%;  Score 30;  DB 22;  Length 9;
  Best Local Similarity   57.1%;  Pred. No. 9.3e+05;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ||: |
Db          1 WFDITNW 7


RESULT 12
ABP24040
ID   ABP24040 standard; Peptide; 9 AA.
```

XX
AC ABP24040;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A24 motif env peptide #6.
XX
KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
KW antigen; vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1 -
XX
PS Claim 32; Page 362; 448pp; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
CC may be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 9 AA;

Query Match 49.2%; Score 30; DB 22; Length 9;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| ||: |
Db 1 WFDITNW 7

RESULT 13
AAP40008
ID AAP40008 standard; peptide; 5 AA.
XX
AC AAP40008;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 04-FEB-1992 (first entry)
XX
DE Sequence of gastric secretion inhibitor.
XX
KW Gastric secretion inhibitor; gastro-duodenal ulcer therapy.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "bonded to H, a protecing gp. for the
FT terminal amine, such as tert.-butoxy-
FT carbonyl (Boc), benzyloxy-carbonyl
FT (Z) or lower alkanoyl"
FT Modified-site 5
FT /label= Asp-NH2
XX
PN EP124420-A.
XX
PD 07-NOV-1984.
XX
PF 19-APR-1984; 84EP-0400787.
XX
PR 20-APR-1983; 83FR-0006492.
XX
PA (SNFI) SANOFI SA.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Martinez J, Ball JP, Castro BL, Nisato D, Demarne H;
XX
DR WPI; 1984-277632/45.
XX
PT Polypeptide gastric secretion inhibitors - for treating
PT gastro-duodenal ulcers
XX
PS Claim 5; Page 16; 17pp; French.
XX
CC The peptides of the invention are gastric secretion inhibitors used
CC for treatment of gastro-duodenal ulcers. They are administered
CC parenterally in doses of 1-100 mg/kg.
CC (Updated on 09-JAN-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 5 AA;

Query Match 47.5%; Score 29; DB 5; Length 5;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
| |||
Db 1 YGWMD 5

RESULT 14
AAP40033
ID AAP40033 standard; peptide; 7 AA.
XX
AC AAP40033;
XX
DT 25-MAR-2003 (updated)
DT 09-JAN-2003 (updated)
DT 04-FEB-1992 (first entry)
XX
DE Sequence of gastric secretion inhibitor.
XX
KW Gastric secretion inhibitor; gastro-duodenal ulcer therapy.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers

FT Modified-site 1
FT /label= benzyloxycarbonyl-Glu
FT Modified-site 7
FT /label= Asp-NH2
XX
PN EP124420-A.
XX
PD 07-NOV-1984.
XX
PF 19-APR-1984; 84EP-0400787.
XX
PR 20-APR-1983; 83FR-0006492.
XX
PA (SNFI) SANOFI SA.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Martinez J, Ball JP, Castro BL, Nisato D, Demarne H;
XX
DR WPI; 1984-277632/45.
XX
PT Polypeptide gastric secretion inhibitors - for treating
PT gastro-duodenal ulcers
XX
PS Claim 6; Page 16; 17pp; French.
XX
CC The peptides of the invention are gastric secretion inhibitors used
CC for treatment of gastro-duodenal ulcers. They are administered
CC parenterally in doses of 1-100 mg/kg.
CC (Updated on 09-JAN-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 7 AA;

Query Match 47.5%; Score 29; DB 5; Length 7;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
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Db 3 YGWMD 7

RESULT 15
AAP50373
ID AAP50373 standard; Peptide; 7 AA.
XX
AC AAP50373;
XX
DT 08-MAR-1992 (first entry)
XX
DE Gastric acid secretion and pancreatic exocrine promoting peptide.
XX
KW Gastric acid secretion; pancreatic exocrine.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 2
FT /label= Tyr(SO3H)
XX
PN JP59222458-A.
XX
PD 14-DEC-1984.
XX
PF 31-MAY-1983; 83JP-0097718.
XX
PR 31-MAY-1983; 83JP-0097718.
XX
PA (AMAN) AMANO PHARM KK.
XX
DR WPI; 1985-027847/05.
XX
PT Novel peptide - having gastric acid secretion promoting and
PT pancreatic exocrine-promoting activity.
XX
PS Example 1; Page 3; 5pp; Japanese.
XX
CC The peptide has a glutaryl gp at the N-terminal; the C-terminal is
CC amidated. The peptide displayed a gastric acid-promoting specific
CC activity 6.1 fold greater than that of tetragastrin 1.
CC See also AAP50348 (generic) and AAP50374 (specific example).
XX
SQ Sequence 7 AA;

Query Match 47.5%; Score 29; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
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Db 2 YGWMD 6

Search completed: August 4, 2003, 12:22:53
Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:22:11 ; Search time 16 Seconds
(without alignments)
23.800 Million cell updates/sec

Title: US-09-103-808-2
Perfect score: 61
Sequence: 1 YSWMDISCW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 77717

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	61	100.0	9	4	US-09-103-808-2	Sequence 2, Appli
3	50	82.0	8	2	US-08-723-116-3	Sequence 3, Appli
4	50	82.0	8	4	US-09-103-808-3	Sequence 3, Appli
5	41	67.2	7	2	US-08-723-116-4	Sequence 4, Appli
6	41	67.2	7	4	US-09-103-808-4	Sequence 4, Appli
7	30	49.2	7	1	US-08-431-539-9	Sequence 9, Appli
8	29	47.5	6	1	US-08-431-539-11	Sequence 11, Appl
9	29	47.5	7	1	US-08-431-539-15	Sequence 15, Appl
10	29	47.5	8	1	US-08-178-570-44	Sequence 44, Appl
11	29	47.5	8	3	US-08-369-643-44	Sequence 44, Appl
12	29	47.5	8	5	PCT-US95-00147-44	Sequence 44, Appl
13	29	47.5	9	1	US-08-178-570-69	Sequence 69, Appl
14	29	47.5	9	3	US-08-369-643-69	Sequence 69, Appl
15	29	47.5	9	5	PCT-US95-00147-69	Sequence 69, Appl
16	27	44.3	8	3	US-09-082-279B-1480	Sequence 1480, Ap
17	27	44.3	8	4	US-09-315-304B-1634	Sequence 1634, Ap
18	27	44.3	8	4	US-09-834-784-1480	Sequence 1480, Ap
19	27	44.3	9	1	US-08-526-710-13	Sequence 13, Appl
20	27	44.3	9	3	US-08-862-855-13	Sequence 13, Appl
21	27	44.3	9	3	US-09-226-985-13	Sequence 13, Appl
22	27	44.3	9	4	US-09-227-906-13	Sequence 13, Appl
23	27	44.3	9	4	US-09-311-784A-222	Sequence 222, App
24	26	42.6	7	3	US-09-059-111-16	Sequence 16, Appl
25	26	42.6	7	3	US-09-059-111-39	Sequence 39, Appl
26	26	42.6	7	5	PCT-US95-08353-16	Sequence 16, Appl
27	26	42.6	7	5	PCT-US95-08353-39	Sequence 39, Appl
28	26	42.6	8	1	US-08-271-830-55	Sequence 55, Appl
29	26	42.6	9	3	US-09-258-754-64	Sequence 64, Appl
30	26	42.6	9	3	US-09-042-107-64	Sequence 64, Appl
31	25	41.0	6	3	US-09-059-111-24	Sequence 24, Appl
32	25	41.0	6	5	PCT-US95-08353-24	Sequence 24, Appl
33	25	41.0	8	1	US-08-190-788A-18	Sequence 18, Appl
34	25	41.0	8	1	US-08-383-474B-23	Sequence 23, Appl
35	25	41.0	8	1	US-08-465-391A-18	Sequence 18, Appl
36	25	41.0	8	2	US-08-464-538B-18	Sequence 18, Appl
37	25	41.0	8	2	US-08-463-076E-62	Sequence 62, Appl
38	24.5	40.2	8	3	US-08-907-403A-4	Sequence 4, Appli
39	24	39.3	5	2	US-08-559-492-6	Sequence 6, Appli
40	24	39.3	5	2	US-08-757-316C-28	Sequence 28, Appl
41	24	39.3	7	2	US-08-310-912A-134	Sequence 134, App
42	24	39.3	7	3	US-08-827-171B-13	Sequence 13, Appl
43	24	39.3	7	3	US-09-301-085-134	Sequence 134, App
44	24	39.3	7	4	US-09-588-995A-111	Sequence 111, App
45	24	39.3	7	5	PCT-US95-04589-134	Sequence 134, App

ALIGNMENTS

```
RESULT 1
US-08-723-116-2
; Sequence 2, Application US/08723116
; Patent No. 5837248
;  GENERAL INFORMATION:
;    APPLICANT:  KIKUCHI, KOKICHI
;    APPLICANT:  SATO, NORIYUKI
;    APPLICANT:  SAHARA, HIROMITSU
;    APPLICANT:  YASOJIMA, TAKAHIRO
;    APPLICANT:  WADA, YOSHIMASA
;    APPLICANT:  SUZUKI, MANABU
;    APPLICANT:  HAMURO, JUNJI
;    TITLE OF INVENTION:  PEPTIDE CAPABLE OF INDUCING IMMUNE
;    TITLE OF INVENTION:  RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;    TITLE OF INVENTION:  OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,116
;      FILING DATE:  30-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 253491/1995
;      FILING DATE:  29-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 217140/1996
;      FILING DATE:  19-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-821-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN
US-08-723-116-2

  Query Match             100.0%;  Score 61;  DB 2;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISCW 9
              |||||||||
Db          1 YSWMDISCW 9


RESULT 2
US-09-103-808-2
; Sequence 2, Application US/09103808
; Patent No. 6368852
;   GENERAL INFORMATION:
;        APPLICANT: KIKUCHI, KOKICHI
;                   SATO, NORIYUKI
;                   SAHARA, HIROMITSU
;                   YASOJIMA, TAKAHIRO
;                   WADA, YOSHIMASA
;                   SUZUKI, MANABU
;                   HAMURO, JUNJI
;        TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
;                            RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;                            OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;                        P.C.
;             STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;             CITY: ARLINGTON
;             STATE: VA
;             COUNTRY: USA
;             ZIP: 22202
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/103,808
;             FILING DATE: 24-Jun-1998
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/723,116
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: JP 217140/1996
;             FILING DATE: 19-AUG-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: OBLON, NORMAN F.
;             REGISTRATION NUMBER: 24,618
;             REFERENCE/DOCKET NUMBER: 10-821-0X
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 703-413-3000
;             TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 9 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        ORIGINAL SOURCE:
;             ORGANISM: HUMAN
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-103-808-2

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  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISCW 9
              |||||||||
Db          1 YSWMDISCW 9


RESULT 3
US-08-723-116-3
; Sequence 3, Application US/08723116
; Patent No. 5837248
;  GENERAL INFORMATION:
;    APPLICANT:  KIKUCHI, KOKICHI
;    APPLICANT:  SATO, NORIYUKI
;    APPLICANT:  SAHARA, HIROMITSU
;    APPLICANT:  YASOJIMA, TAKAHIRO
;    APPLICANT:  WADA, YOSHIMASA
;    APPLICANT:  SUZUKI, MANABU
;    APPLICANT:  HAMURO, JUNJI
;    TITLE OF INVENTION:  PEPTIDE CAPABLE OF INDUCING IMMUNE
;    TITLE OF INVENTION:  RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;    TITLE OF INVENTION:  OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/723,116
;      FILING DATE:  30-SEP-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 253491/1995
;      FILING DATE:  29-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 217140/1996
;      FILING DATE:  19-AUG-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OBLON, NORMAN F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  10-821-0X
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-413-3000
;      TELEFAX:  703-413-2220
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    ORIGINAL SOURCE:
;      ORGANISM:  HUMAN
US-08-723-116-3

  Query Match             82.0%;  Score 50;  DB 2;  Length 8;
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Qy          1 YSWMDISC 8
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Db          1 YSWMDISC 8
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RESULT 4
US-09-103-808-3
; Sequence 3, Application US/09103808
; Patent No. 6368852
;  GENERAL INFORMATION:
;       APPLICANT: KIKUCHI, KOKICHI
;                  SATO, NORIYUKI
;                  SAHARA, HIROMITSU
;                  YASOJIMA, TAKAHIRO
;                  WADA, YOSHIMASA
;                  SUZUKI, MANABU
;                  HAMURO, JUNJI
;       TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
;                           RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;                           OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;                       P.C.
;            STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;            CITY: ARLINGTON
;            STATE: VA
;            COUNTRY: USA
;            ZIP: 22202
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
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;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/103,808
;            FILING DATE: 24-Jun-1998
;            CLASSIFICATION: <Unknown>
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;            APPLICATION NUMBER: 08/723,116
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: JP 217140/1996
;            FILING DATE: 19-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: OBLON, NORMAN F.
;            REGISTRATION NUMBER: 24,618
;            REFERENCE/DOCKET NUMBER: 10-821-0X
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 703-413-3000
;            TELEFAX: 703-413-2220
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 8 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       ORIGINAL SOURCE:
;            ORGANISM: HUMAN
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-103-808-3

  Query Match             82.0%;  Score 50;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDISC 8
              ||||||||
Db          1 YSWMDISC 8


RESULT 5
US-08-723-116-4
; Sequence 4, Application US/08723116
; Patent No. 5837248
;  GENERAL INFORMATION:
;       APPLICANT:  KIKUCHI, KOKICHI
;       APPLICANT:  SATO, NORIYUKI
;       APPLICANT:  SAHARA, HIROMITSU
;       APPLICANT:  YASOJIMA, TAKAHIRO
;       APPLICANT:  WADA, YOSHIMASA
;       APPLICANT:  SUZUKI, MANABU
;       APPLICANT:  HAMURO, JUNJI
;       TITLE OF INVENTION:  PEPTIDE CAPABLE OF INDUCING IMMUNE
;       TITLE OF INVENTION:  RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
;       TITLE OF INVENTION:  OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
;       NUMBER OF SEQUENCES:  4
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;         ADDRESSEE:  P.C.
;         STREET:  1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
;         CITY:  ARLINGTON
;         STATE:  VA
;         COUNTRY:  USA
;         ZIP:  22202
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  US/08/723,116
;         FILING DATE:  30-SEP-1996
;         CLASSIFICATION:  530
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;         APPLICATION NUMBER:  JP 253491/1995
;         FILING DATE:  29-SEP-1995
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER:  JP 217140/1996
;         FILING DATE:  19-AUG-1996
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  OBLON, NORMAN F.
;         REGISTRATION NUMBER:  24,618
;         REFERENCE/DOCKET NUMBER:  10-821-0X
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  703-413-3000
;         TELEFAX:  703-413-2220
;     INFORMATION FOR SEQ ID NO:  4:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  7 amino acids
;         TYPE:  amino acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  peptide
;       ORIGINAL SOURCE:
;         ORGANISM:  HUMAN
US-08-723-116-4

  Query Match             67.2%;  Score 41;  DB 2;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWMDIS 7
              |||||||
Db          1 YSWMDIS 7


RESULT 6
US-09-103-808-4
; Sequence 4, Application US/09103808
; Patent No. 6368852
;  GENERAL INFORMATION:
;       APPLICANT: KIKUCHI, KOKICHI
;                  SATO, NORIYUKI
;                  SAHARA, HIROMITSU
;                  YASOJIMA, TAKAHIRO
;                  WADA, YOSHIMASA
;                  SUZUKI, MANABU
;                  HAMURO, JUNJI
```

; TITLE OF INVENTION: PEPTIDE CAPABLE OF INDUCING IMMUNE
; RESPONSE TO HUMAN GASTRIC CANCER AND AGENT FOR PREVENTING
; OR TREATING HUMAN GASTRIC CANCER, CONTAINING THE PEPTIDE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,808
; FILING DATE: 24-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/723,116
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 217140/1996
; FILING DATE: 19-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-821-0X
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-103-808-4

Query Match 67.2%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 YSWMDIS 7
              |||||||
Db          1 YSWMDIS 7
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RESULT 7
US-08-431-539-9
; Sequence 9, Application US/08431539
; Patent No. 5580751
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Breddam, Klaus
; APPLICANT: Henriksen, Dennis
; TITLE OF INVENTION: Process for the Preparation of
; TITLE OF INVENTION: C-Terminally Amidated Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5580751west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,539
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,306
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-431-539-9

Query Match 49.2%; Score 30; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 YSWMDIS 7
              | |||  :
Db          1 YGWMDFA 7
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RESULT 8
US-08-431-539-11
; Sequence 11, Application US/08431539
; Patent No. 5580751
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Breddam, Klaus
; APPLICANT: Henriksen, Dennis
; TITLE OF INVENTION: Process for the Preparation of
; TITLE OF INVENTION: C-Terminally Amidated Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5580751west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,539
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,306
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081

; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-431-539-11

Query Match 47.5%; Score 29; DB 1; Length 6;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
| |||
Db 1 YGWMD 5

RESULT 9
US-08-431-539-15
; Sequence 15, Application US/08431539
; Patent No. 5580751
; GENERAL INFORMATION:
; APPLICANT: Buchardt, Ole
; APPLICANT: Breddam, Klaus
; APPLICANT: Henriksen, Dennis
; TITLE OF INVENTION: Process for the Preparation of
; TITLE OF INVENTION: C-Terminally Amidated Peptides
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5580751west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,539
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,306
; FILING DATE: 15-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nelson, Albin J.
; REGISTRATION NUMBER: 28,650
; REFERENCE/DOCKET NUMBER: 9663.8-US-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-431-539-15

Query Match 47.5%; Score 29; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
| |||
Db 1 YGWMD 5

RESULT 10
US-08-178-570-44
; Sequence 44, Application US/08178570
; Patent No. 5532167
; GENERAL INFORMATION:
; APPLICANT: Lewis C. Cantley
; APPLICANT: Zhou Song yang
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/178,570
; FILING DATE: JANUARY 7, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-178-570-44

Query Match 47.5%; Score 29; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
| |||
Db 4 YGWMD 8

RESULT 11
US-08-369-643-44
; Sequence 44, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
; APPLICANT: Cantley, Lewis C.
; APPLICANT: Songyang, Zhou
; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; FILE REFERENCE: CNS-001CP
; CURRENT APPLICATION NUMBER: US/08/369,643A
; CURRENT FILING DATE: 1995-01-06
; EARLIER APPLICATION NUMBER: US 08/178,570
; EARLIER FILING DATE: 1994-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:gastrin
US-08-369-643-44

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  Query Match             47.5%;  Score 29;  DB 3;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
              | |||
Db          4 YGWMD 8


RESULT 12
PCT-US95-00147-44
; Sequence 44, Application PC/TUS9500147
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Substrate Specificity of Protein Kinases
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00147
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/178,570
;      FILING DATE:  JANUARY 7, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A., Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-004CPPC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
PCT-US95-00147-44

  Query Match             47.5%;  Score 29;  DB 5;  Length 8;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
              | |||
Db          4 YGWMD 8


RESULT 13
US-08-178-570-69
; Sequence 69, Application US/08178570
; Patent No. 5532167
;  GENERAL INFORMATION:
;    APPLICANT:  Lewis C. Cantley
;    APPLICANT:  Zhou Song yang
;    TITLE OF INVENTION:  Substrate Specificity of Protein Kinases
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, suite 510
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109-1875
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII text
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/178,570
;      FILING DATE:  JANUARY 7, 1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeConti, Giulio A., Jr.
;      REGISTRATION NUMBER:  31,503
;      REFERENCE/DOCKET NUMBER:  BBI-004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-08-178-570-69

  Query Match             47.5%;  Score 29;  DB 1;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
              | |||
Db          5 YGWMD 9


RESULT 14
US-08-369-643-69
; Sequence 69, Application US/08369643A
; Patent No. 6004757
; GENERAL INFORMATION:
;  APPLICANT: Cantley, Lewis C.
;  APPLICANT: Songyang, Zhou
;  TITLE OF INVENTION: Substrate Specificity of Protein Kinases
;  FILE REFERENCE: CNS-001CP
;  CURRENT APPLICATION NUMBER: US/08/369,643A
;  CURRENT FILING DATE: 1995-01-06
;  EARLIER APPLICATION NUMBER: US 08/178,570
;  EARLIER FILING DATE: 1994-01-07
;  NUMBER OF SEQ ID NOS: 92
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Gastrin
US-08-369-643-69

  Query Match             47.5%;  Score 29;  DB 3;  Length 9;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+05;
  Matches    4;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
              | |||
Db          5 YGWMD 9


RESULT 15
PCT-US95-00147-69
; Sequence 69, Application PC/TUS9500147
;  GENERAL INFORMATION:
;    APPLICANT:
```

; TITLE OF INVENTION: Substrate Specificity of Protein Kinases
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 STATE STREET, suite 510
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/00147
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,570
; FILING DATE: JANUARY 7, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A., Jr.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: BBI-004CPPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-00147-69

Query Match 47.5%; Score 29; DB 5; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 YSWMD 5
              | |||
Db          5 YGWMD 9
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Search completed: August 4, 2003, 12:24:33
Job time : 17 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:22:57 ; Search time 21 Seconds
(without alignments)
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Title: US-09-103-808-2
Perfect score: 61
Sequence: 1 YSWMDISCW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 46290

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	39.3	6	10	US-09-847-940B-12	Sequence 12, Appl
2	24	39.3	6	10	US-09-982-704-9	Sequence 9, Appli
3	24	39.3	6	11	US-09-847-946A-12	Sequence 12, Appl
4	24	39.3	6	11	US-09-847-946A-95	Sequence 95, Appl
5	24	39.3	7	10	US-09-867-852-134	Sequence 134, App
6	24	39.3	7	10	US-09-884-767A-10	Sequence 10, Appl
7	24	39.3	7	11	US-09-847-946A-99	Sequence 99, Appl
8	24	39.3	8	11	US-09-847-946A-92	Sequence 92, Appl
9	24	39.3	8	11	US-09-847-946A-100	Sequence 100, App
10	24	39.3	9	9	US-09-765-086-197	Sequence 197, App
11	24	39.3	9	11	US-09-847-946A-91	Sequence 91, Appl
12	24	39.3	9	11	US-09-847-946A-94	Sequence 94, Appl
13	24	39.3	9	11	US-09-847-946A-97	Sequence 97, Appl
14	24	39.3	9	11	US-09-847-946A-98	Sequence 98, Appl
15	24	39.3	9	15	US-10-272-411-27	Sequence 27, Appl
16	24	39.3	9	15	US-10-272-328A-27	Sequence 27, Appl
17	24	39.3	9	15	US-10-264-374-197	Sequence 197, App
18	24	39.3	9	15	US-10-219-850-6	Sequence 6, Appli
19	23	37.7	6	10	US-09-765-614B-9	Sequence 9, Appli
20	23	37.7	6	10	US-09-925-715-6	Sequence 6, Appli
21	23	37.7	6	10	US-09-865-018-11	Sequence 11, Appl
22	23	37.7	8	10	US-09-791-378-429	Sequence 429, App
23	23	37.7	9	15	US-10-165-762A-8	Sequence 8, Appli
24	23	37.7	9	15	US-10-165-762A-9	Sequence 9, Appli
25	23	37.7	9	15	US-10-165-762A-12	Sequence 12, Appl
26	22	36.1	5	11	US-09-962-298-8	Sequence 8, Appli
27	22	36.1	6	15	US-10-304-160-5	Sequence 5, Appli
28	22	36.1	7	10	US-09-945-249-50	Sequence 50, Appl
29	22	36.1	7	10	US-09-945-249-51	Sequence 51, Appl
30	22	36.1	7	10	US-09-945-249-58	Sequence 58, Appl
31	22	36.1	7	10	US-09-945-249-61	Sequence 61, Appl
32	22	36.1	7	10	US-09-945-249-63	Sequence 63, Appl
33	22	36.1	7	10	US-09-945-249-67	Sequence 67, Appl
34	22	36.1	7	10	US-09-945-249-73	Sequence 73, Appl
35	22	36.1	7	11	US-09-281-495-29	Sequence 29, Appl
36	22	36.1	7	11	US-09-972-656-41	Sequence 41, Appl
37	22	36.1	8	9	US-09-863-971A-5	Sequence 5, Appli
38	22	36.1	8	10	US-09-864-011A-5	Sequence 5, Appli
39	22	36.1	8	11	US-09-962-298-7	Sequence 7, Appli
40	22	36.1	8	11	US-09-880-748-2740	Sequence 2740, Ap
41	22	36.1	8	11	US-09-981-206A-5	Sequence 5, Appli
42	22	36.1	8	11	US-09-981-271A-5	Sequence 5, Appli
43	22	36.1	8	15	US-10-094-401-174	Sequence 174, App
44	22	36.1	9	8	US-08-424-550B-373	Sequence 373, App
45	22	36.1	9	9	US-09-288-326-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-847-940B-12
; Sequence 12, Application US/09847940B
; Patent No. US20020156000A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J.
; APPLICANT: Ghosh, Sankar
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-117CP
; CURRENT APPLICATION NUMBER: US/09/847,940B
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD mutants
US-09-847-940B-12

Query Match 39.3%; Score 24; DB 10; Length 6;
Best Local Similarity 75.0%; Pred. No. 4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWM 4
|||:
Db 3 YSWL 6

RESULT 2
US-09-982-704-9
; Sequence 9, Application US/09982704
; Publication No. US20020192795A1
; GENERAL INFORMATION:
; APPLICANT: KIY, THOMAS

; APPLICANT: SCHULTZ, JOACHIM
; TITLE OF INVENTION: CATHEPSIN-L, ITS PREPRO FORM AND THE CORRESPONDING
; TITLE OF INVENTION: PROPEPTIDE FROM CILIATES
; FILE REFERENCE: 514489-3898
; CURRENT APPLICATION NUMBER: US/09/982,704
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 08/981,957
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: PCT/EP97/02388
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 19619366.4
; PRIOR FILING DATE: 1996-05-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Paramecium tetraurelia
US-09-982-704-9

Query Match 39.3%; Score 24; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SCW 9
|||
Db 3 SCW 5

RESULT 3
US-09-847-946A-12
; Sequence 12, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NBD peptide
US-09-847-946A-12

Query Match 39.3%; Score 24; DB 11; Length 6;
Best Local Similarity 75.0%; Pred. No. 4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWM 4
|||:
Db 3 YSWL 6

RESULT 4
US-09-847-946A-95
; Sequence 95, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-95

Query Match 39.3%; Score 24; DB 11; Length 6;
Best Local Similarity 75.0%; Pred. No. 4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWM 4
|||:
Db 3 YSWL 6

RESULT 5
US-09-867-852-134
; Sequence 134, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; TITLE OF INVENTION: DETECTION METHODS
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-134

Query Match 39.3%; Score 24; DB 10; Length 7;
Best Local Similarity 42.9%; Pred. No. 4e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
::|||:|:
Db 1 FLDIACF 7

RESULT 6

US-09-884-767A-10
; Sequence 10, Application US/09884767A
; Publication No. US20020192789A1
; GENERAL INFORMATION:
; APPLICANT: DYAX Corp.
; APPLICANT: Ley, Arthur C.
; APPLICANT: Luneau, Christopher J.
; APPLICANT: Ladner, Robert C
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT
; CURRENT APPLICATION NUMBER: US/09/884,767A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 09/597,321
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic enterokinase cleavage sequence
US-09-884-767A-10

Query Match 39.3%; Score 24; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YSWMD 5
| | |
Db 1 YEWQD 5

RESULT 7
US-09-847-946A-99
; Sequence 99, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 99
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-99

Query Match 39.3%; Score 24; DB 11; Length 7;
Best Local Similarity 75.0%; Pred. No. 4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWM 4
|||:
Db 3 YSWL 6

RESULT 8
US-09-847-946A-92
; Sequence 92, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-92

Query Match 39.3%; Score 24; DB 11; Length 8;
Best Local Similarity 75.0%; Pred. No. 4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWM 4
|||:
Db 5 YSWL 8

RESULT 9
US-09-847-946A-100
; Sequence 100, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
; APPLICANT: May, Michael J
; APPLICANT: Ghosh, Sankar
; APPLICANT: Findeis, Mark A
; APPLICANT: Phillips, Kathryn
; APPLICANT: Hannig, Gerhard
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
; FILE REFERENCE: PPI-119
; CURRENT APPLICATION NUMBER: US/09/847,946A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,261
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 09/643,260
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 100
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
; OTHER INFORMATION: sequence
US-09-847-946A-100

Query Match 39.3%; Score 24; DB 11; Length 8;
Best Local Similarity 75.0%; Pred. No. 4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YSWM 4
|||:
Db 3 YSWL 6

```
RESULT 10
US-09-765-086-197
; Sequence 197, Application US/09765086
; Patent No. US20010046498A1
; GENERAL INFORMATION:
;  APPLICANT: Ruoslahti, Erkki
;  APPLICANT:  Pasqualini, Renata
;  APPLICANT:  Wadih, Arap
;  APPLICANT:  Bredesen, Dale E.
;  APPLICANT:  Ellerby, H. Michael
;  TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
;  TITLE OF INVENTION:  Pro-Apoptotic Activity
;  FILE REFERENCE: P-LJ 3844
;  CURRENT APPLICATION NUMBER: US/09/765,086
;  CURRENT FILING DATE:  2001-01-17
;  PRIOR APPLICATION NUMBER: US 09/489,582
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 235
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 197
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic peptide
US-09-765-086-197

  Query Match             39.3%;  Score 24;  DB 9;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SCW 9
              |||
Db          7 SCW 9


RESULT 11
US-09-847-946A-91
; Sequence 91, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
;  APPLICANT: May, Michael J
;  APPLICANT:  Ghosh, Sankar
;  APPLICANT:  Findeis, Mark A
;  APPLICANT:  Phillips, Kathryn
;  APPLICANT:  Hannig, Gerhard
;  TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;  FILE REFERENCE: PPI-119
;  CURRENT APPLICATION NUMBER: US/09/847,946A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,261
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: 09/643,260
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 91
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
;   OTHER INFORMATION: sequence
US-09-847-946A-91

  Query Match             39.3%;  Score 24;  DB 11;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWM 4
              |||:
Db          3 YSWL 6
```

```
RESULT 12
US-09-847-946A-94
; Sequence 94, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
;  APPLICANT: May, Michael J
;  APPLICANT:  Ghosh, Sankar
;  APPLICANT:  Findeis, Mark A
;  APPLICANT:  Phillips, Kathryn
;  APPLICANT:  Hannig, Gerhard
;  TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;  FILE REFERENCE: PPI-119
;  CURRENT APPLICATION NUMBER: US/09/847,946A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,261
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: 09/643,260
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
;   OTHER INFORMATION: sequence
US-09-847-946A-94

  Query Match             39.3%;  Score 24;  DB 11;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWM 4
              |||:
Db          3 YSWL 6


RESULT 13
US-09-847-946A-97
; Sequence 97, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
;  APPLICANT: May, Michael J
;  APPLICANT:  Ghosh, Sankar
;  APPLICANT:  Findeis, Mark A
;  APPLICANT:  Phillips, Kathryn
;  APPLICANT:  Hannig, Gerhard
;  TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;  FILE REFERENCE: PPI-119
;  CURRENT APPLICATION NUMBER: US/09/847,946A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,261
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: 09/643,260
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
;   OTHER INFORMATION: sequence
US-09-847-946A-97

  Query Match             39.3%;  Score 24;  DB 11;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 YSWM 4
              |||:
Db          5 YSWL 8
```

```
RESULT 14
US-09-847-946A-98
; Sequence 98, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
;  APPLICANT: May, Michael J
;  APPLICANT:  Ghosh, Sankar
;  APPLICANT:  Findeis, Mark A
;  APPLICANT:  Phillips, Kathryn
;  APPLICANT:  Hannig, Gerhard
;  TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;  FILE REFERENCE: PPI-119
;  CURRENT APPLICATION NUMBER: US/09/847,946A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,261
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: 09/643,260
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:NEMO binding
;   OTHER INFORMATION: sequence
US-09-847-946A-98
```

```
  Query Match             39.3%;  Score 24;  DB 11;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 4e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSWM 4
              |||:
Db          4 YSWL 7
```

```
RESULT 15
US-10-272-411-27
; Sequence 27, Application US/10272411
; Publication No. US20030100068A1
; GENERAL INFORMATION:
;  APPLICANT: Barnes Jewish Hospital
;  APPLICANT:  Lam, Jonathan
;  APPLICANT:  Ross, F. Patrick
;  APPLICANT:  Teitelbaum, Steven
;  TITLE OF INVENTION: RANKL MIMICS AND USES THEREOF
;  FILE REFERENCE: 60019620-0202
;  CURRENT APPLICATION NUMBER: US/10/272,411
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/329,393
;  PRIOR FILING DATE: 2001-10-15
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-272-411-27
```

```
  Query Match             39.3%;  Score 24;  DB 15;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 SCW 9
              |||
Db          1 SCW 3
```

```
Search completed: August  4, 2003, 12:25:00
Job time : 21 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:21:46 ; Search time 15 Seconds
(without alignments)
57.701 Million cell updates/sec

Title: US-09-103-808-2
Perfect score: 61
Sequence: 1 YSWMDISCW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	44.3	7	2	S33244	neuromodulatory pe
2	27	44.3	7	2	S33245	neuromodulatory pe
3	25	41.0	7	2	S33246	neuromodulatory pe
4	23	37.7	9	2	C57444	neuropeptide Grb-A
5	23	37.7	9	2	PT0272	Ig heavy chain CRD
6	22	36.1	5	2	A32516	cholecystokinin-5
7	22	36.1	8	2	PQ0012	cholecystokinin -
8	22	36.1	8	2	A43001	cholecystokinin -
9	22	36.1	8	2	JS0318	leucokinin VIII -
10	22	36.1	9	2	A61357	phyllocaerulein -
11	21.5	35.2	9	1	AKLQIM	locustamyoinhibiti
12	21	34.4	6	2	PD0028	pev-kinin 2 - pena
13	20	32.8	9	2	A57444	neuropeptide Grb-A
14	19	31.1	9	2	B57444	neuropeptide Grb-A
15	18	29.5	6	2	B34835	dnaA protein - Pse
16	18	29.5	9	2	PT0270	Ig heavy chain CRD
17	17	27.9	6	2	A31263	dihydrofolate redu
18	17	27.9	6	2	B35640	cerebellar degener
19	17	27.9	8	2	C61512	variant surface gl
20	17	27.9	8	2	JS0316	leucokinin VI - Ma
21	16	26.2	7	2	A61081	tryptophyllin, bas
22	16	26.2	8	2	T13818	cytochrome oxidase
23	15	24.6	4	2	PT0661	T-cell receptor be
24	15	24.6	5	2	PT0580	T-cell receptor be
25	15	24.6	6	2	A61068	locustakinin - mig
26	15	24.6	7	2	PN0649	pullulanase (EC 3.
27	15	24.6	8	2	S10596	adipokinetic hormo
28	15	24.6	8	2	D61512	variant surface gl
29	15	24.6	8	2	JS0315	leucokinin V - Mad
30	15	24.6	8	2	JS0317	leucokinin VII - M
31	15	24.6	8	2	A38887	T-cell receptor ga
32	15	24.6	9	2	A24244	adipokinetic hormo
33	15	24.6	9	2	D57444	neuropeptide Grb-A
34	15	24.6	9	2	PT0299	Ig heavy chain CRD
35	15	24.6	9	2	I58350	gene c-mpl protein
36	14	23.0	6	2	B31263	dihydrofolate redu
37	14	23.0	6	2	PT0519	T-cell receptor be
38	14	23.0	7	2	S57274	triacylglycerol li
39	14	23.0	7	2	PH1602	Ig H chain V-D-J r
40	14	23.0	7	2	PT0586	T-cell receptor be
41	14	23.0	7	2	PC2370	probable H+-transp
42	14	23.0	7	4	A58725	virotoxin - destro
43	14	23.0	8	2	A31570	angiotensin-conver
44	14	23.0	8	2	PC1002	leucine-tRNA ligas
45	14	23.0	9	2	I46023	growth hormone rec

ALIGNMENTS

RESULT 1
S33244
neuromodulatory peptide WWamide-1 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33244
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33244
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 44.3%; Score 27; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 WMDISCW 9
              | ::| |
Db          1 WKEMSVW 7
```

RESULT 2
S33245
neuromodulatory peptide WWamide-2 - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33245
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33245
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 44.3%; Score 27; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 WMDISCW 9
              | ::| |
Db          1 WREMSVW 7
```

RESULT 3
S33246
neuromodulatory peptide WWamide-3 - giant African snail
C;Species: Achatina fulica (giant African snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: S33246
R;Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
FEBS Lett. 323, 104-108, 1993
A;Title: WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t
A;Reference number: S33244; MUID:93265912; PMID:8495720
A;Accession: S33246
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MIN>

Query Match 41.0%; Score 25; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 WMDISCW 9
| :| |
Db 1 WKQMSVW 7

RESULT 4
C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: C57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 37.7%; Score 23; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SWMDIS 7
:| |:|
Db 1 AWRDLS 6

RESULT 5
PT0272
Ig heavy chain CRD3 region (clone 3-103B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0272
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0272
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 37.7%; Score 23; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YSWMD 5
|:| |
Db 1 YNWND 5

RESULT 6
A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and in
A;Reference number: A32516; MUID:87153871; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecy
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.1%; Score 22; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WMD 5
|||
Db 2 WMD 4

RESULT 7
PQ0012
cholecystokinin - southeastern quoll
N;Alternate names: CCK
C;Species: Dasyurus viverrinus (southeastern quoll)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C;Accession: PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: PQ0012
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 36.1%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WMD 5
|||
Db 5 WMD 7

RESULT 8
A43001
cholecystokinin - tammar wallaby
N;Alternate names: CCK
C;Species: Macropus eugenii (tammar wallaby)
C;Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 13-Sep-1996
C;Accession: A43001; PQ0012
R;Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A;Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A;Reference number: PQ0012; MUID:88234141; PMID:3375140
A;Accession: A43001
A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 36.1%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 WMD 5
              |||
Db          5 WMD 7
```

RESULT 9
JS0318
leucokinin VIII - Madeira cockroach
C;Species: Leucophaea maderae (Madeira cockroach)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: JS0318
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fir
A;Reference number: JS0317
A;Accession: JS0318
A;Molecule type: protein
A;Residues: 1-8 <HOL>
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C;Keywords: amidated carboxyl end; cephalomyotropic peptide
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.1%; Score 22; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 YSW 3
              |||
Db          5 YSW 7
```

RESULT 10
A61357
phyllocaerulein - Sauvage's leaf frog
C;Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C;Accession: A61357
R;Anastasi, A.; Bertaccini, G.; Cei, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
Br. J. Pharmacol. 37, 198-206, 1969
A;Title: Structure and pharmacological actions of phyllocaerulein, a caerulein-like nona
A;Reference number: A61357; MUID:70005484; PMID:5824931
A;Accession: A61357
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ANA>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Binding site: sulfate (Tyr) (covalent) #status experimental
F;9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.1%; Score 22; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 WMD 5
              |||
Db          6 WMD 8
```

RESULT 11
AKLQIM
locustamyoinhibiting peptide - migratory locust
C;Species: Locusta migratoria (migratory locust)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998
C;Accession: A60065
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Regul. Pept. 36, 111-119, 1991
A;Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI
A;Reference number: A60065; MUID:92179466; PMID:1796179
A;Accession: A60065
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Comment: This peptide hormone suppresses spontaneous contractions of the hindgut a
C;Superfamily: locustamyoinhibiting peptide
C;Keywords: amidated carboxyl end; hormone
F;9/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 35.2%; Score 21.5; DB 1; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

```
Qy          2 SWMDISC-W 9
              :| |::  |
Db          1 AWQDLNAGW 9
```

RESULT 12
PD0028
pev-kinin 2 - penaeid shrimp (Penaeus vannamei) (fragment)
C;Species: Penaeus vannamei
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C;Accession: PD0028
R;Nieto, J.; Veelaert, D.; Derua, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devree
Biochem. Biophys. Res. Commun. 248, 406-411, 1998
A;Title: Identification of one tachykinin- and two kinin-related peptides in the brai
A;Reference number: PD0027; MUID:98342103; PMID:9675150
A;Accession: PD0028
A;Molecule type: protein
A;Residues: 1-6 <NIE>
C;Comment: This peptide belongs to myotropic neuropeptides.

Query Match 34.4%; Score 21; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 DISCW 9
              | | |
Db          1 DFSAW 5
```

RESULT 13
A57444
neuropeptide Grb-AST B1 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: A57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: A57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 32.8%; Score 20; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 WMDIS 7
              | |::
Db          2 WQDLN 6
```

RESULT 14
B57444
neuropeptide Grb-AST B2 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: B57444
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the

A;Reference number: A57444; MUID:95403341; PMID:7673141
A;Accession: B57444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>

Query Match 31.1%; Score 19; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          3 WMDIS 7
              | |::
Db          2 WRDLN 6
```

RESULT 15
B34835
dnaA protein - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
C;Accession: B34835
R;Yee, T.W.; Smith, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
A;Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from Es
A;Reference number: A34835; MUID:90160310; PMID:2106132
A;Accession: B34835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-6 <YEE>
A;Cross-references: GB:M30125; NID:g151419; PIDN:AAA25916.1; PID:g151421
C;Keywords: DNA binding

Query Match 29.5%; Score 18; DB 2; Length 6;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 MDISCW 9
              | :  |
Db          1 MSVELW 6
```

Search completed: August 4, 2003, 12:24:10
Job time : 15 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:21:01 ; Search time 11 Seconds
(without alignments)
38.476 Million cell updates/sec

Title: US-09-103-808-2
Perfect score: 61
Sequence: 1 YSWMDISCW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	44.3	7	1	WWA1_ACHFU	P35919 achatina fu
2	27	44.3	7	1	WWA3_ACHFU	P35921 achatina fu
3	25	41.0	7	1	WWA2_ACHFU	P35920 achatina fu
4	24.5	40.2	9	1	PTSP_BOMMO	P82003 bombyx mori
5	22	36.1	8	1	CCKN_MACEU	P30369 macropus eu
6	22	36.1	8	1	LCK8_LEUMA	P19990 leucophaea
7	21.5	35.2	9	1	LMIP_LOCMI	P31799 locusta mig
8	17	27.9	8	1	LCK4_LEUMA	P21143 leucophaea
9	17	27.9	8	1	LCK6_LEUMA	P19988 leucophaea
10	16	26.2	6	1	EI01_LITRU	P82096 litoria rub
11	15	24.6	4	1	OCP3_OCTMI	P58649 octopus min
12	15	24.6	6	1	LOK1_LOCMI	P41491 locusta mig
13	15	24.6	8	1	AKH_LIBAU	P25418 libellula a
14	15	24.6	8	1	LCK1_LEUMA	P21140 leucophaea
15	15	24.6	8	1	LCK2_LEUMA	P21141 leucophaea
16	15	24.6	8	1	LCK3_LEUMA	P21142 leucophaea
17	15	24.6	8	1	LCK5_LEUMA	P19987 leucophaea
18	15	24.6	8	1	LCK7_LEUMA	P19989 leucophaea
19	14	23.0	8	1	ACI_THUAL	P18691 thunnus alb
20	13	21.3	7	1	TPFY_PACDA	P83455 pachymedusa
21	13	21.3	8	1	AL16_CARMA	P81819 carcinus ma
22	13	21.3	9	1	D1_NEPNO	P24816 nephrops no
23	13	21.3	9	1	OXYT_BUFRE	P42995 bufo regula
24	12	19.7	5	1	AL14_CARMA	P81817 carcinus ma
25	12	19.7	5	1	UF01_MOUSE	P38639 mus musculu
26	12	19.7	7	1	BRHP_CONIM	P58803 conus imper
27	12	19.7	8	1	AL15_CARMA	P81818 carcinus ma
28	12	19.7	8	1	AL17_CARMA	P81820 carcinus ma
29	12	19.7	8	1	AL18_CARMA	P81821 carcinus ma
30	12	19.7	8	1	ALL3_CYDPO	P82154 cydia pomon
31	12	19.7	8	1	ALL4_CALVO	P41840 calliphora
32	12	19.7	8	1	ALL4_CYDPO	P82155 cydia pomon
33	12	19.7	8	1	HTF1_PERAM	P04548 periplaneta
34	12	19.7	8	1	HTF2_PERAM	P04549 periplaneta
35	12	19.7	8	1	HTF_TENMO	P25419 tenebrio mo
36	12	19.7	8	1	RT34_BOVIN	P82929 bos taurus
37	12	19.7	9	1	RE42_LITRU	P82075 litoria rub
38	12	19.7	9	1	TAL1_PICJA	P17440 pichia jadi
39	12	19.7	9	1	TAL3_PICJA	P17441 pichia jadi
40	11	18.0	5	1	BPP7_BOTIN	P30425 bothrops in
41	11	18.0	7	1	TY51_LITRU	P82065 litoria rub
42	11	18.0	8	1	ACT_CARMA	P80709 carcinus ma
43	11	18.0	8	1	AKHG_GRYBI	P14086 gryllus bim
44	11	18.0	8	1	AKH_MELML	P25423 melolontha
45	11	18.0	8	1	AKH_TABAT	P14595 tabanus atr

ALIGNMENTS

RESULT 1
WWA1_ACHFU
ID WWA1_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WWamide-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel *neuro*modulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 44.3%; Score 27; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 1.3e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 WMDISCW 9
              | ::| |
Db          1 WREMSVW 7
```

RESULT 2
WWA3_ACHFU
ID WWA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WWamide-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).

```
DR   PIR; S33244; S33244.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  965 MW;  7362D5B69B132310 CRC64;

  Query Match             44.3%;  Score 27;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              | ::| |
Db          1 WKEMSVW 7


RESULT 3
WWA2_ACHFU
ID   WWA2_ACHFU     STANDARD;      PRT;      7 AA.
AC   P35920;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   01-OCT-1994 (Rel. 30, Last annotation update)
DE   WWamide-2.
OS   Achatina fulica (Giant African snail).
OC   Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC   Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX   NCBI_TaxID=6530;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Ganglion;
RX   MEDLINE=93265912; PubMed=8495720;
RA   Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT   "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from
RT   ganglia of the African giant snail, Achatina fulica.";
RL   FEBS Lett. 323:104-108(1993).
DR   PIR; S33246; S33246.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  964 MW;  7362D5B686D32310 CRC64;

  Query Match             41.0%;  Score 25;  DB 1;  Length 7;
  Best Local Similarity   42.9%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              |  :| |
Db          1 WKQMSVW 7


RESULT 4
PTSP_BOMMO
ID   PTSP_BOMMO     STANDARD;      PRT;      9 AA.
AC   P82003;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prothoracicostatic peptide (Bom-PTSP).
OS   Bombyx mori (Silk moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
OC   Bombycidae; Bombyx.
OX   NCBI_TaxID=7091;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=C145 X N140; TISSUE=Brain;
RX   MEDLINE=20002634; PubMed=10531308;
RA   Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA   Kataoka H.;
RT   "Identification of a prothoracicostatic peptide in the larval brain of
RT   the silkworm, Bombyx mori.";
RL   J. Biol. Chem. 274:31169-31173(1999).
RN   [2]
RP   ERRATUM.
RA   Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Nagata S.,
RA   Kataoka H.;
RL   J. Biol. Chem. 275:9892-9892(2000).
CC   -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
CC       gland.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
KW   Hormone; Amidation.
FT   MOD_RES       9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  1090 MW;  3878C5B4472AB6C3 CRC64;

  Query Match             40.2%;  Score 24.5;  DB 1;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 SWMDI-SCW 9
              :| |: | |
Db          1 AWQDLNSAW 9


RESULT 5
CCKN_MACEU
ID   CCKN_MACEU     STANDARD;      PRT;      8 AA.
AC   P30369;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Cholecystokinin (CCK).
GN   CCK.
OS   Macropus eugenii (Tammar wallaby), and
OS   Dasyurus viverrinus (Southeastern quoll).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX   NCBI_TaxID=9315, 9279;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=M.eugenii, and D.viverrinus;
RC   TISSUE=Brain;
RX   MEDLINE=88234141; PubMed=3375140;
RA   Fan Z.W., Eng J., Shaw G., Yalow R.S.;
RT   "Cholecystokinin octapeptide purified from brains of Australian
RT   marsupials.";
RL   Peptides 9:429-431(1988).
CC   -!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
CC       AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
CC       IN THE BRAIN IS NOT CLEAR.
CC   -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR   PIR; A43001; A43001.
DR   PIR; PQ0012; PQ0012.
DR   InterPro; IPR001651; Gastrin.
DR   PROSITE; PS00259; GASTRIN; 1.
KW   Amidation; Sulfation; Hormone.
FT   MOD_RES       2       2       SULFATION.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  1064 MW;  DDCAA68378768B5A CRC64;

  Query Match             36.1%;  Score 22;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WMD 5
              |||
Db          5 WMD 7


RESULT 6
LCK8_LEUMA
ID   LCK8_LEUMA     STANDARD;      PRT;      8 AA.
AC   P19990;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   01-FEB-1991 (Rel. 17, Last annotation update)
DE   Leucokinin VIII (L-VIII).
OS   Leucophaea maderae (Madeira cockroach).
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OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure and synthesis of leucokinins VII and
RT   VIII: the final members of this new family of cephalomyotropic
RT   peptides isolated from head extracts of Leucophaea maderae.";
RL   Comp. Biochem. Physiol. 88C:31-34(1987).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
DR   PIR; JS0318; JS0318.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  902 MW;  736365AB59CAADD8 CRC64;

  Query Match             36.1%;  Score 22;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              |||
Db          5 YSW 7


RESULT 7
LMIP_LOCMI
ID   LMIP_LOCMI     STANDARD;      PRT;      9 AA.
AC   P31799;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   01-OCT-1993 (Rel. 27, Last annotation update)
DE   Locustamyoinhibiting peptide (LOM-MIP).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92179466; PubMed=1796179;
RA   Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT   "Isolation, identification and synthesis of locustamyoinhibiting
RT   peptide (LOM-MIP), a novel biologically active neuropeptide from
RT   Locusta migratoria.";
RL   Regul. Pept. 36:111-119(1991).
CC   -!- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
CC       OVIDUCT.
CC   -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
CC       IN THE SUBOESOPHAGEAL GANGLION.
DR   PIR; A60065; AKLQIM.
KW   Amidation; Neuropeptide.
FT   MOD_RES       9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  1060 MW;  387D7DD4472AB6C3 CRC64;

  Query Match             35.2%;  Score 21.5;  DB 1;  Length 9;
  Best Local Similarity   33.3%;  Pred. No. 1.3e+05;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          2 SWMDISC-W 9
              :| |::  |
Db          1 AWQDLNAGW 9


RESULT 8
LCK4_LEUMA
ID   LCK4_LEUMA     STANDARD;      PRT;      8 AA.
AC   P21143;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-MAY-1991 (Rel. 18, Last annotation update)
DE   Leucokinin IV (L-IV).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Primary structure and synthesis of two additional neuropeptides
RT   from Leucophaea maderae: members of a new family of
RT   Cephalomyotropins.";
RL   Comp. Biochem. Physiol. 84C:271-276(1986).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  906 MW;  DC6365B1E9D5BDDA CRC64;

  Query Match             27.9%;  Score 17;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              :||
Db          5 HSW 7


RESULT 9
LCK6_LEUMA
ID   LCK6_LEUMA     STANDARD;      PRT;      8 AA.
AC   P19988;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Leucokinin VI (L-VI).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Head;
RX   MEDLINE=87052651; PubMed=2877794;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure, and synthesis of leucokinins V and VI:
RT   myotropic peptides of Leucophaea maderae.";
RL   Comp. Biochem. Physiol. 88C:27-30(1987).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS, AND TO MANDUCA SEXTA AND
CC       HELIOTHIS ZEA ADIPOKINETIC HORMONE.
DR   PIR; JS0316; JS0316.
KW   Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  935 MW;  9D6365B1E9D5A5A6 CRC64;

  Query Match             27.9%;  Score 17;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 YSW 3
              :||
Db          5 HSW 7


RESULT 10
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EI01_LITRU
ID   EI01_LITRU     STANDARD;      PRT;     6 AA.
AC   P82096;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Electrin 1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
KW   Amphibian defense peptide; Amidation.
FT   MOD_RES       6      6       AMIDATION.
SQ   SEQUENCE   6 AA;  792 MW;  6683704772C9A000 CRC64;

  Query Match             26.2%;  Score 16;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WM 4
              ||
Db          5 WM 6


RESULT 11
OCP3_OCTMI
ID   OCP3_OCTMI     STANDARD;      PRT;     4 AA.
AC   P58649;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cardioactive peptides Ocp-3/Ocp-4.
OS   Octopus minor (Octopus).
OC   Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
OC   Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
OX   NCBI_TaxID=89766;
RN   [1]
RP   SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC   TISSUE=Brain;
RX   MEDLINE=20336815; PubMed=10876044;
RA   Iwakoshi E., Hisada M., Minakata H.;
RT   "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT   Octopus minor.";
RL   Peptides 21:623-630(2000).
CC   -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC       inotropic effects on the heart. Ocp-4 is a 1000 time less
CC       active than Ocp-3.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC   -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW   Hormone; D-amino acid.
FT   MOD_RES       2      2       D-SERINE (IN OCP-4).
SQ   SEQUENCE   4 AA;  463 MW;  6AB365B810000000 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 4;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SW 3
              ||
Db          2 SW 3


RESULT 12
LOK1_LOCMI
ID   LOK1_LOCMI     STANDARD;      PRT;     6 AA.
AC   P41491;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Locustakinin I.
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=92262851; PubMed=1585017;
RA   Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,
RA   de Loof A.;
RT   "Locustakinin, a novel myotropic peptide from Locusta migratoria,
RT   isolation, primary structure and synthesis.";
RL   Regul. Pept. 37:49-57(1992).
CC   -!- FUNCTION: Myotropic peptide. May be important in the stimulation
CC       of ion transport and inhibition of diuretic activity in Malpighian
CC       tubules.
CC   -!- SUBCELLULAR LOCATION: Secreted.
DR   PIR; A61068; A61068.
KW   Neuropeptide; Amidation.
FT   MOD_RES       6      6       AMIDATION.
SQ   SEQUENCE   6 AA;  654 MW;  686365A5B9CDB000 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SW 3
              ||
Db          4 SW 5


RESULT 13
AKH_LIBAU
ID   AKH_LIBAU      STANDARD;      PRT;     8 AA.
AC   P25418;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Adipokinetic hormone (AKH).
OS   Libellula auripennis (Skimmer dragonfly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Palaeoptera; Odonata; Anisoptera; Libellulidae; Libellula.
OX   NCBI_TaxID=6966;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90359055; PubMed=2390213;
RA   Gaede G.;
RT   "The putative ancestral peptide of the adipokinetic/red-pigment-
RT   concentrating hormone family isolated and sequenced from a
RT   dragonfly.";
RL   Biol. Chem. Hoppe-Seyler 371:475-483(1990).
CC   -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CC       CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
CC       DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
CC       MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
CC   -!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
DR   PIR; S10596; S10596.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       8      8       AMIDATION.
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SQ   SEQUENCE   8 AA;  978 MW;  8665A771A9C452D6 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SW 3
              ||
Db          7 SW 8


RESULT 14
LCK1_LEUMA
ID   LCK1_LEUMA     STANDARD;      PRT;     8 AA.
AC   P21140;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-MAY-1991 (Rel. 18, Last annotation update)
DE   Leucokinin I (L-I).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure and synthesis of two neuropeptides
RT   from Leucophaea maderae: members of a new family of
RT   Cephalomyotropins.";
RL   Comp. Biochem. Physiol. 84C:205-211(1986).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  893 MW;  DC6365B449CDC76A CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SW 3
              ||
Db          6 SW 7


RESULT 15
LCK2_LEUMA
ID   LCK2_LEUMA     STANDARD;      PRT;     8 AA.
AC   P21141;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-MAY-1991 (Rel. 18, Last sequence update)
DT   01-MAY-1991 (Rel. 18, Last annotation update)
DE   Leucokinin II (L-II).
OS   Leucophaea maderae (Madeira cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC   Blaberidae; Leucophaea.
OX   NCBI_TaxID=6988;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Head;
RA   Holman G.M., Cook B.J., Nachman R.J.;
RT   "Isolation, primary structure and synthesis of two neuropeptides
RT   from Leucophaea maderae: members of a new family of
RT   Cephalomyotropins.";
RL   Comp. Biochem. Physiol. 84C:205-211(1986).
CC   -!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
CC       ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
CC   -!- SIMILARITY: TO THE OTHER LEUCOKININS.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  852 MW;  DC6365A5B9C8676A CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 SW 3
              ||
Db          6 SW 7


Search completed: August  4, 2003, 12:23:10
Job time : 11 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: August 4, 2003, 12:21:21 ; Search time 32 Seconds
(without alignments)
72.577 Million cell updates/sec

Title: US-09-103-808-2
Perfect score: 61
Sequence: 1 YSWMDISCW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 775

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	34.4	8	11	O35835	O35835 rattus sp.
2	20	32.8	8	4	Q15888	Q15888 homo sapien
3	20	32.8	8	6	Q9TRY3	Q9try3 sus sp. ins
4	19	31.1	8	8	Q9T4Y2	Q9t4y2 asterina pe
5	19	31.1	9	2	Q8GL31	Q8gl31 borrelia bu
6	19	31.1	9	2	Q8GL26	Q8gl26 borrelia bu
7	19	31.1	9	4	Q16386	Q16386 homo sapien
8	17	27.9	8	4	Q9Y4X6	Q9y4x6 homo sapien
9	17	27.9	8	11	Q9ET18	Q9et18 mus spretus
10	17	27.9	8	11	Q9ET17	Q9et17 mus caroli
11	17	27.9	8	11	Q9ET16	Q9et16 mesocricetu
12	17	27.9	9	8	Q94XE6	Q94xe6 tectocoris
13	16	26.2	7	10	O49223	O49223 glycine max
14	16	26.2	8	4	Q15890	Q15890 homo sapien
15	16	26.2	9	1	Q50832	Q50832 methanococc
16	16	26.2	9	8	Q94VC6	Q94vc6 varanus pil
17	15	24.6	7	15	Q8JE81	Q8je81 human immun
18	15	24.6	8	2	O85406	O85406 coxiella bu
19	15	24.6	8	4	Q9BYY5	Q9byy5 homo sapien
20	15	24.6	8	5	P82685	P82685 periplaneta
21	15	24.6	8	5	P82686	P82686 periplaneta
22	15	24.6	8	5	P82687	P82687 periplaneta
23	15	24.6	8	5	P82688	P82688 periplaneta
24	15	24.6	8	5	P82689	P82689 periplaneta
25	15	24.6	8	6	Q9BF82	Q9bf82 ursus arcto
26	15	24.6	8	6	Q9BFC2	Q9bfc2 macropus eu
27	15	24.6	8	6	Q9BF90	Q9bf90 tragelaphus
28	15	24.6	8	6	Q9BFB1	Q9bfb1 echinops te
29	15	24.6	8	6	Q9BF93	Q9bf93 megaptera n
30	15	24.6	8	6	Q9BFA1	Q9bfa1 ateles fusc
31	15	24.6	8	6	Q9BF87	Q9bf87 tapirus ind
32	15	24.6	8	6	Q9BFB9	Q9bfb9 euphractus
33	15	24.6	8	6	Q9BFB8	Q9bfb8 chaetophrac
34	15	24.6	8	6	Q9BFA0	Q9bfa0 macaca mula
35	15	24.6	8	6	Q9BFA8	Q9bfa8 loxodonta a
36	15	24.6	8	6	Q9BFA9	Q9bfa9 procavia ca
37	15	24.6	8	6	Q9BFB2	Q9bfb2 sorex arane
38	15	24.6	8	6	Q9BFB5	Q9bfb5 erinaceus c
39	15	24.6	8	6	Q9BFB6	Q9bfb6 myrmecophag
40	15	24.6	8	6	Q9BFB3	Q9bfb3 condylura c
41	15	24.6	8	6	Q9BF88	Q9bf88 equus cabal
42	15	24.6	8	6	Q9BF95	Q9bf95 rousettus l
43	15	24.6	8	6	Q9BF99	Q9bf99 hylobates c
44	15	24.6	8	6	Q9BF84	Q9bf84 panthera on
45	15	24.6	8	6	Q9BFC3	Q9bfc3 didelphis m

ALIGNMENTS

RESULT 1
O35835
ID O35835 PRELIMINARY; PRT; 8 AA.
AC O35835;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF1 protein.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=98008057; PubMed=9581555;
RA Hospital V., Prat A., Joulie C., Cherif D., Day R., Cohen P.;
RT "Human and rat testis express two mRNA species encoding varients of
RT NRD convertase, a metalloendopeptidase of the insulinase family.";
RL Biochem. J. 327:773-779(1997).
DR EMBL; X93208; CAA63695.1; -.
SQ SEQUENCE 8 AA; 886 MW; EA7EA1B1ADC5A5B6 CRC64;

Query Match 34.4%; Score 21; DB 11; Length 8;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 SCW 9
              :||
Db          6 TCW 8
```

RESULT 2
Q15888
ID Q15888 PRELIMINARY; PRT; 8 AA.
AC Q15888;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

```
DE   (Clone XP15H8A) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32069; AAA73878.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1068 MW;  0315A37EAB5B0763 CRC64;

  Query Match             32.8%;  Score 20;  DB 4;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CW 9
              ||
Db          5 CW 6


RESULT 3
Q9TRY3
ID   Q9TRY3      PRELIMINARY;      PRT;     8 AA.
AC   Q9TRY3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Insulin-like growth factor-binding protein-6, IGFBP-6 (Fragment).
OS   Sus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9826;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92049376; PubMed=1719383;
RA   Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT   "Isolation and molecular cloning of insulin-like growth factor-binding
RT   protein-6.";
RL   Mol. Endocrinol. 5:938-948(1991).
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  850 MW;  9FB2CEA37EA7687D CRC64;

  Query Match             32.8%;  Score 20;  DB 6;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CW 9
              ||
Db          4 CW 5


RESULT 4
Q9T4Y2
ID   Q9T4Y2      PRELIMINARY;      PRT;     8 AA.
AC   Q9T4Y2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   COI gene product (Fragment).
OS   Asterina pectinifera (Starfish).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;
OC   Asteroidea; Valvatacea; Valvatida; Asterinidae; Asterina.
OX   NCBI_TaxID=7594;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89354669; PubMed=2766382;
RA   Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.;
RT   "Conserved tRNA gene cluster in starfish mitochondrial DNA.";
RL   Curr. Genet. 15:193-206(1989).
DR   EMBL; X16886; CAA34767.1; -.
KW   Mitochondrion.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1114 MW;  F0C9D36415B736D6 CRC64;

  Query Match             31.1%;  Score 19;  DB 8;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 8.3e+05;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISCW 9
              | :| |
Db          1 MQLSRW 6


RESULT 5
Q8GL31
ID   Q8GL31      PRELIMINARY;      PRT;     9 AA.
AC   Q8GL31;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   PF-50 protein (Fragment).
GN   PF-50.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OG   Plasmid group cp32-1.
OC   Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sh-2-82;
RA   Stevenson B., Miller J.C.;
RT   "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT   prophages: conservation amidst diversity.";
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY142089; AAN17869.1; -.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  1206 MW;  5A4A244337204373 CRC64;

  Query Match             31.1%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWM 4
              | |:
Db          1 YKWI 4


RESULT 6
Q8GL26
ID   Q8GL26      PRELIMINARY;      PRT;     9 AA.
AC   Q8GL26;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   PF-50 protein (Fragment).
GN   PF-50.
OS   Borrelia burgdorferi (Lyme disease spirochete).
OG   Plasmid group cp32-5.
OC   Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX   NCBI_TaxID=139;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sh-2-82;
RA   Stevenson B., Miller J.C.;
RT   "Comparative analyses of Borrelia burgdorferi erp genes and their cp32
RT   prophages: conservation amidst diversity.";
```

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RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY142092; AAN17873.1; -.
KW   Plasmid.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  1206 MW;  5A4A244330504373 CRC64;

  Query Match             31.1%;  Score 19;  DB 2;  Length 9;
  Best Local Similarity   50.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 YSWM 4
              | |:
Db          1 YKWI 4


RESULT 7
Q16386
ID   Q16386      PRELIMINARY;      PRT;     9 AA.
AC   Q16386;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Mex40 protein (Fragment).
GN   MEX40.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95400293; PubMed=7670464;
RA   Budarf M.L., Collins J., Gong W., Roe B., Wang Z., Bailey L.C.,
RA   Sellinger B., Michaud D., Driscoll D.A., Emanuel B.S.;
RT   "Cloning a balanced translocation associated with DiGeorge syndrome
RT   and identification of a disrupted candidate gene.";
RL   Nat. Genet. 10:269-278(1995).
DR   EMBL; S79485; AAD14301.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  1137 MW;  734911A69446837B CRC64;

  Query Match             31.1%;  Score 19;  DB 4;  Length 9;
  Best Local Similarity   40.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 WMDIS 7
              ||:::
Db          3 WMNMT 7


RESULT 8
Q9Y4X6
ID   Q9Y4X6      PRELIMINARY;      PRT;     8 AA.
AC   Q9Y4X6;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Nuclear LIM interactor (Fragment).
GN   NLI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20108806; PubMed=10640831;
RA   Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler S.,
RA   Schroth A., Bodem J., Royer-Pokora B.;
RT   "Genomic structure, alternative transcripts and chromosome location of
RT   the human LIM domain binding protein gene LDB1.";
RL   Cytogenet. Cell Genet. 87:119-124(1999).
DR   EMBL; AJ243097; CAB45408.1; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  767 MW;  EE6EBDDEB862D5B6 CRC64;

  Query Match             27.9%;  Score 17;  DB 4;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 MDISC 8
              | : |
Db          1 MSVGC 5


RESULT 9
Q9ET18
ID   Q9ET18      PRELIMINARY;      PRT;     8 AA.
AC   Q9ET18;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Neuropeptide Y (Fragment).
OS   Mus spretus (Western wild mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10096;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRET/Ei;
RA   Taylor B.A., Wnek C., Phillips S.J.;
RT   "Multiple obesity QTLs identified in an intercross between the NZO
RT   (New Zealand obese) and the SM (small) mouse strains.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF286200; AAG01474.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1033 MW;  297685A76AAB1734 CRC64;

  Query Match             27.9%;  Score 17;  DB 11;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 8.3e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 DISCW 9
              | | |
Db          4 DPSMW 8


RESULT 10
Q9ET17
ID   Q9ET17      PRELIMINARY;      PRT;     8 AA.
AC   Q9ET17;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Neuropeptide Y (Fragment).
OS   Mus caroli (Wild mouse) (Ricefield mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10089;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Taylor B.A., Wnek C., Phillips S.J.;
RT   "Multiple obesity QTLs identified in an intercross between the NZO
RT   (New Zealand obese) and the SM (small) mouse strains.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF286201; AAG01475.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1033 MW;  297685A76AAB1734 CRC64;

  Query Match             27.9%;  Score 17;  DB 11;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 8.3e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 DISCW 9
              | | |
Db          4 DPSMW 8
```

```
RESULT 11
Q9ET16
ID   Q9ET16      PRELIMINARY;      PRT;     8 AA.
AC   Q9ET16;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   Neuropeptide Y (Fragment).
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Taylor B.A., Wnek C., Phillips S.J.;
RT   "Multiple obesity QTLs identified in an intercross between the NZO
RT   (New Zealand obese) and the SM (small) mouse strains.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF286202; AAG01476.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1033 MW;  297685A76AAB1734 CRC64;

  Query Match             27.9%;  Score 17;  DB 11;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 8.3e+05;
  Matches    3;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 DISCW 9
              | | |
Db          4 DPSMW 8


RESULT 12
Q94XE6
ID   Q94XE6      PRELIMINARY;      PRT;     9 AA.
AC   Q94XE6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Cytochrome c oxidase subunit III (Fragment).
GN   COX3.
OS   Tectocoris diophthalmus (cotton harlequin bug).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC   Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC   Tectocoris.
OX   NCBI_TaxID=159956;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21396409; PubMed=11504862;
RA   Shao R., Campbell N.J.H., Schmidt E.R., Barker S.C.;
RT   "Increased rate of gene rearrangement in the mitochondrial genomes of
RT   three orders of hemipteroid insects.";
RL   Mol. Biol. Evol. 18:1828-1832(2001).
DR   EMBL; AF335990; AAK55283.1; -.
KW   Mitochondrion.
FT   NON_TER       1      1
SQ   SEQUENCE   9 AA;  1206 MW;  A2C563636B5041A6 CRC64;

  Query Match             27.9%;  Score 17;  DB 8;  Length 9;
  Best Local Similarity   42.9%;  Pred. No. 8.3e+05;
  Matches    3;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 WMDISCW 9
              :| |  |
Db          1 YMTIYWW 7


RESULT 13
O49223
ID   O49223      PRELIMINARY;      PRT;     7 AA.
AC   O49223;
DT   01-JUN-1998 (TrEMBLrel. 06, Created)
DT   01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HMG-1-like protein (Fragment).
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Essex; TISSUE=Root;
RX   MEDLINE=91367679; PubMed=1891369;
RA   Laux T., Goldberg R.B.;
RT   "A plant DNA binding protein shares highly conserved sequence motifs
RT   with HMG-box proteins.";
RL   Nucleic Acids Res. 19:4769-4769(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Essex; TISSUE=Root;
RA   Mahalingam R., Knap H.T.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF047050; AAC03556.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  850 MW;  6AAAAAB378637810 CRC64;

  Query Match             26.2%;  Score 16;  DB 10;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 YSWMD 5
              : | |
Db          2 WGWDD 6


RESULT 14
Q15890
ID   Q15890      PRELIMINARY;      PRT;     8 AA.
AC   Q15890;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (Clone XP19G12A) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32083; AAA73880.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  975 MW;  605EA6C5BEA5A2D3 CRC64;

  Query Match             26.2%;  Score 16;  DB 4;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 8.3e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 ISC 8
              :||
Db          2 VSC 4


RESULT 15
Q50832
ID   Q50832      PRELIMINARY;      PRT;     9 AA.
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AC   Q50832;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DE   Intergenic AT-rich DNA sequence (Fragment).
OS   Methanococcus voltae.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanococcaceae; Methanococcus.
OX   NCBI_TaxID=2188;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85230552; PubMed=4006907;
RA   Bollschweiler C., Kuehn R., Klein A.;
RT   "Non-repetitive AT-rich sequences are found in intergenic regions of
RT   Methanococcus voltae DNA.";
RL   EMBO J. 4:805-809(1985).
DR   EMBL; X02518; CAA26355.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1087 MW;  99ED005DC404405A CRC64;

  Query Match             26.2%;  Score 16;  DB 1;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 8.3e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 MDIS 7
              |||:
Db          1 MDIN 4


Search completed: August  4, 2003, 12:23:50
Job time : 33 secs
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